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## Replacement Sheet

**Figure 1**

ID-65

Clone 3-60

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(SEQ ID NO: 1)

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GTGTTTATGATGAAAAAAGGACAAGTAAATGATACTAAGCAA  
TCTTACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAA  
TTTTAGGGTCATTTCATAATGGTCACAAGTCCTGTTTTTGCGGA  
TCAAACACATCGGTTCAAGTTAATAATCAGACAGGCACTAG  
TGTGGATGCTAATAATTCTTCCAATGAGACAAGTGCGTCAAGT  
GTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGATAAAG  
TTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC  
CTTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTG  
AACAAGGGAATTATGTTTATAGCAAAGAAACCGAGGTGAAAA  
ATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAAAGA  
AAGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATA  
ATGTGAAATGGATTTTCATATAAGTCTTTTGGTGGCGTACGTCG  
ATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCA  
GACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAA  
TCAAGAGAAAATAGCAACGCAAGGAAATTATACATTTTCA  
TAAAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAGTCCAA  
CTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACC  
AAATACTAATACTATTGAAGGAAATCAGTGGTTATCTTATAAATC  
ATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGCATCTT  
CAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAAC  
CACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAA  
CGAAACAATACTACAGGTTTTGATATTTTAATTACGAATATTAAA  
GATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTGGACTG  
AACAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTAA  
CTACTGGGGATGGCAACTACAAAGTAGCTGTATCATTGCTG  
ACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACTA  
CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAA  
AGTGACAGTAGCTGGAACATAATTCTTCTCAAGAACCTATTGA  
AAATGGTTTACCAAAGACTGGTGTTTATAATATTATCGGAAGT  
ACTGAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCAA  
TTTACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTA  
TTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATCTTATA  
GTGGTGTTCGTCGCTATATTCTGTGAAAAAGCTAACTACAAG  
TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTA  
TCCCAACTTACCTAAAACAGGTACCTATACATTTACTAAAAC  
GTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCAGTGGAA  
TTTAATTTTCAAAAGGGTGAAAAAATACATTATGATCAAGTGT

TAGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTC  
CGGTATTCGTCGCTATATTGAAATTAA

5 (SEQ ID NO: 2)  
MFMMKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNN  
QTGTSVDANNSSNETSASSVITSNNDSVQASDKVVNSQNTATKDITPLVETK  
PMVEKTLPEQGNVYYSKETEVKNTPSKSAPVAFYAKKGDKVFDQVFNKDN  
10 VKWISYKSFGGVRRYAAIESLDPSGGSETKAPTPVTNSGSNNQEKIATQGNYT  
FSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYKSFNGVRRFV  
LLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFDILITNIKDDNGIA  
AVKVPVWTEQGGQDDIKWYTAVTGDNKYKVAVSFADHKNEKGLYNIHLY  
YQEASGTLVGVGTGKVTVAGTNSSQEPIENGLPKTG VYNIIGSTEVKNEAKISS  
15 QTQFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKD  
EATKPTSYPNLPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVV  
DGHQWISYKSYSGIRRYIEI\*

Sequence description  
20 A) Length: 1642 bp - 547 aa (full length gene)  
B) Sequence Characteristics:  
Potential leader peptide sequence  
Orf is preceded by a potential Shine-  
Dalgarno sequence.

25 ID-66

Clone 3-5

30 (SEQ ID NO: 3)  
ATGATATTGAGACGTCGAACTATTGTTTTATGGCAACTGGGTATCGCCATT  
TCTCTCATTCTTAGTATTCTAGCCTTAAATCTTTATTTCCATAGTACTCCCTT  
GCAAACCAATGCAGCTTTACGGAACCTTGCTCCTTCATTAAACCATCTTTT  
TGGGACAGATGGTTTAGGTAGGGATATGTTTGTGAGAACGATTAAAGGAC  
35 TTTATTTCTCTCTACAAGTCGGCTTATTAGGTGCCCTTATGGGGGTCATTCT  
GGCGACAGTTTTTGGAGTGCTTGCAGGTTTAGGAAATAGCATTATTGATAA  
AATAATAGCATGGTTAGTTGATTTGTTTATTGGTATGCCTCATTTGATTTTT  
ATGATTCTCATTTCTTTTGTGTTGGGAAAGGTGCTCAAGGGGTCATCATT  
GCAACGGCTGTTACACATTGGCCTTCTTTAGCAAGGCTTATCCGCAATGAA  
40 GTCTATCATCTAAAGAATAAAGAATTTGTCCAACCTTTCTAAAAGTATGGGA  
AAAACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTC  
AAATTTTCATTGGTTTTATCCTCTTATTTCCACATGTCATCCTACATGAAGC  
ATCAATGACTTTCTTAGGATTTGGGCTCTCTGCCGAACAACCTTCGGTTGG  
TATCATTCTGTCAGAGGCAGCTAAGCATATCTCTCTTGGAATTGGTGGTT

GGTTATCTTTCCAGGACTTTATCTTATTTTGGTTGTCAATGCATTTGATACT  
ATCGGAGAATCTTTAAAGAACTCTTTTACCCTCAAACCTGATCATTTTTAG

5 (SEQ ID NO: 4)  
MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAAPSLNHLFGTD  
GLGRDMFVRTIKGLYFSLQVGLLGALMGVILATVFGVLAGLGNSIIDKIIAWL  
VDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKE  
FVQLSKSMGKTPYYIVRHILPLIASQIFIGILLFPHVILHEASMTFLGFGLSAE  
10 QPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF  
\*

Sequence description

15 A) Length: 822 bp - 274 aa (full length gene)  
B) Sequence Characteristics:  
Potential leader peptide sequence  
Orf is preceded by a potential Shine-  
20 Dalgarno sequence.

ID-78

25 Clone 3-5b

(SEQ ID NO: 5)  
ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTTCACTCAA  
TACGGAAGATTTTTTAAAACCATTTCAATCAACACCGATACAAGCGCTGA  
30 ATTTAGAAATTAAAAAAGGTGAGTTATTAGCTATTATAGGTGCTAGTGGTT  
CGGGGAAGAGTTTATTAGCACATGCTATTATGGATATTCTTCCTAAAAATG  
CATCTGTAACAGGAGATATGATTTATCGTGGTCAATCACTAAATTCTAAAC  
GCATTAAACAGTTGCGAGGAAAAGATATTACGTTGATTCCACAATCAGTT  
AATTATTTAGATCCATCTATGAAAGTCAAACATCAGGTGCGCTTAGGTATC  
35 TCAGAAAATTCAAAGGCTACTCAAGAAGGATTGTTTCAACAGTTTGGTTTA  
AAAGAAAGTGATGGTGACTTGGATCCTTTCCAACCTTTCTGGCGGAATGCTC  
CGACGTGTTTTGTTTACAACGTGTATTAGTGATAAGGTTTCTTTGATTATTG  
CGGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTTAG  
ACCAACTACGCTCCTTTGCAGATAAAGGAATAAGCGTTATATTTATCACTC  
40 ATGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTTTTAAAG  
AGGGAAAAGCTATTGAAACAGCTCCAGCTAGTTTCTTTAGCGGAAATGGA  
GAGCAGTTACAAACAGAATTTGCTAGAAGTTTATGGCGCTCTCTCCACAG  
CAAGAATTTTTGAAAGGAGTTACTCATGACCTTAGAGGCTAA

(SEQ ID NO: 6)

MTETLLSIKDLSTFTQYGRFLKPFQSTPIQALNLEIKKGELLAIGASGSGKSL  
AHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITLIPQSVNYLDPSMK  
VKHQVRLGISENSKATQEGFLFQQFGLKESDGDLDPFQLSGGMLRRVLFTTCIS  
DKVSLIIADEPTPGLHPDALQMVLDQLRSFADKGISVIFITHDIVAASQIADRITI  
FKEGKAIETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTHDLRG\*

10 Sequence description

A) Length: 804 bp - 268 aa (full length gene)

B) Sequence Characteristics:

No obvious leader peptide sequence

Orf is preceded by a potential Shine-Dalgarno sequence.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified downstream and fully sequenced.

ID-79

25 Clone 3-5c

(SEQ ID NO: 7)

GTCCATCTGGGGTGGTTCCCGATTGGTATTTCTTCTCCGATAGGTACTTTGA  
GTCAAGATATTACGTTAGCTGATCGTATTAAGCACCTTATTTTACCTGTTTT  
CACGGTAAGTATTCTAGGCATTGCCAATGTAACCTTTCATACTAGAACTAA  
AATGATGTCGGTACTTTCTAGTGAATATGTCTTATTTGCCAGAGCGCGTGG  
GGAAACGGAATGGCAAATTTTTTAAAAATCATTGTCTTAGAAATGCTATCGT  
ACCAGCTATTACACTGCATTTTTCCTATTTTGGAGAATTGTTTGGAGGATCC  
GTTCTTGCTGAGCAAGTTTTCTCATATCCAGGACTAGGGTCTACCCTAACT  
GAAGCAGGACTTAAAAGTGATACACCGCTACTTCTAGCTATTGTGATGATA  
GGGACATTATTTGTTTTTGCGGGCAATCTTATTGCGGATATTTTAAATAGC  
ATAATCAATCCACAGTTAAGGAGAAAAGTATGA

(SEQ ID NO: 8)

VHLGWFPIGISSPIGTLSDITLADRIKHLILPVFTVSILGIANVTLHTRTKMMSV  
LSSEYVLFARARGETEWQIFKNHCLRNAIVPAITLHFSYFGELFGGSVLAEQVF  
SYPGLGSTLTEAGLKSDTPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV\*

Sequence description

A) Length: 495 bp - 165 aa (partial gene sequence)

B) Sequence Characteristics:

N-terminus has yet to be determined.

5 This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified upstream.

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ID-80

Clone 2-17

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(SEQ ID NO: 9)

TTGCGGACAATTACGTTCAAACACAATGAAACGCGATCGTCAAAAAGCGA  
AGGTAGGGCGGTAATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGA  
CAAAGATTAGTCGTCGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTAT  
TATTGTCAGGATGTGTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAAC  
20 TCCGAATGTTTCAGCGCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTAA  
TTCTTTTCGTAGTTTAGATCAGCTAACTAGCTTTAAAGAGATTTTTTGGGTT  
ATTGGTCAAAATGTAGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGT  
TACTATCCCTAAAGCCAAGTTTACGGAAATATAAAAGCGTTATATTACTTG  
CTTTCTTGATGTCTCTTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTT  
25 AATAGATGCTAATCGGGTTTTTGAAATCGACGATCTATGGACAAATACCTT  
AGGCGGTCCTTTCGCCCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCT  
AACTATTAGAAAATGA

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(SEQ ID NO: 10)

MRTITFKHNETRSSKSEGRAVMLKRLFTEDGELTKISRRFVWMLVVIYCLIIVR  
MCFGPQIMIEGVSTPNVQRFGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVV  
NILLFPLIIGLLSLKPSLRKYKSVILLAFLMSLFIECTQVVLDILIDANRVFEIDD  
LWTNTLGGPFALWSYRNIKGWLLTIRK\*

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Sequence description

A) Length: 579 bp - 193 aa (full length gene)

B) Sequence Characteristics:

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Possesses a potential leader peptide sequence

No obvious Shine-Dalgarno, but the 'TTG' codon may not be the actual translation start point.

A methionine (ATG) that occurs ~22 codons downstream of the 'TTG' is preceded by a

potential Shine-Dalgarno sequence and may  
represent the actual start codon.

ID 81

5

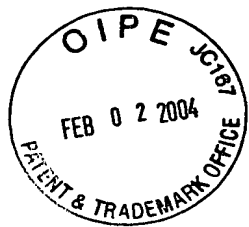
Clone 3-1

(SEQ ID NO: 11)

10 TTGAAAAATTTAAATCGTTATGTAGTTGCGGTTTCTGGAGTCGTTTACATT  
TAATGCTAGGATCAACTTATGCTTGGAGTGTGTTTCGTAACCCAATTATCT  
CAGAGACTGGTTGGGATATTTTCATCAGTTTCATTTCGCTTTTAGTTTGGCTAT  
TTTTTGTCTAGGAATGTCTGCAGCTTTTATGGGACACTTAGTAGAGCGTTT  
GGTCCTAGGATAATGGGAATGATTTCTGCTATTTTATATGGAGCAGGGAAT  
GTGTTAACAGGCTTAGCCATTGAACTCAGCAGTTATGGTTACTGTATGTT  
15 GCATACGGTATTTTAGGAGGAATCGGACTTGGTTCAGGTTATATTACTCCA  
GTATCGACTATTATTAAATGGTTTCCTGATAGGAGGGGACTAGCAACAGG  
ATTCGCTATTATGGGATTTGGCTTTGCTTCTTTAGTAACAAGTCCGCTTGCA  
CAATCCTTACTGATTAGGATTGGTGTGGGTAAAACGTTTTATATTTTGGGA  
TTAGTATATTTTTTTTGTCTATGATGATTGCCTCACAATTTATTAAACAACCAC  
20 CTCAGGAAAAAATAACTATTTTGACTCACGATGGTAAAAAGAATGCTATG  
AATTCACAAATTATCACTGGATTAAAAGCAAACGTCGCTATAAAATCAAA  
AACCTTTTACATCATTTGGTTGACCTTGTTTATTAATATTTTCGTGTGGCTTA  
GGTTTAATATCAGCAGCTTCACCAATGGCACAAGATTTAGCAGGCTATTCC  
GCAGAATCTGCAGCCTTATTAGTAGGGGTACTAGGGATATTTAACGGTTTT  
25 GGACGTCTGTTATGGGCAAGTCTCTCTGACTACATTGGACGCCCGTTGACC  
TTTATAATATTATTTATTGTGAACCTTATTATGACTTCTAGTTTATTTTTGTC  
ATTCAATGCTATTGTATTTGCAATAGCGATGTCTATTTTAATGACTTGTTAT  
GGTGCAGGTTTTTTCCTTATTACCTGCTTATCTAAGTGATATTTTTGGAACAA  
AGGAATTAGCTACTTTACATGGTTATAGTTTAACAGCATGGGCAATAGCAG  
30 GTCTGTTTGGGCCCCCTATTGTTATCAAAGACATATTCATGGGGAAATTCCT  
ATCAATTGACATTAATGGTTTTTGGTTTTTTATTCTTATTCGGATTATTGTTA  
TCTCTATATTTAAGAAAATTAACAACATAAGTTGTGTAG

(SEQ ID NO: 12)

35 LKNLNRYVVAVSGVVLHMLGSTYAWSVFRNPIISETGWDISSVSFAFSLAIFC  
LGMSAAFMGHLVERFGPRIMGMISAILYGAGNVLTGLAIETQQLWLLYVAYG  
ILGGIGLGSYITPVSTIIKWFPDRRLATGFAIMGFGFASLVTSPLAQSLIRIG  
VGKTFYILGLVYFFVMMIASQFIKQPPQEKITILTHDGKKNAMNSQIITGLKAN  
VAIKSKTFYIIWLTLEFINISCGLGLISAASPMQDLAGYSAESAALLVGVLGIFN  
40 GFGRLWASLSDYIGRPLTFIILFIVNFIMTSSLFSLFNAIVFAIAMSILMTCYGA  
GFSLLPAYLSDIFGTKEATLHGYSLTAWAIAGLFGPLLSKTYSWGNSYQLTL  
MVFGFLFLFGLLLSLYLRKLTTKV\*



Sequence description:

5 A] Length 1221 bp - 407 a.a (full length gene).  
B] TTG start codon with Shine-Dalgarno sequence upstream. Obvious signal peptide, with hydropathy plot exhibiting many possible membrane spanning regions, indicating protein to be transmembrane.

10

ID-82

Clone 48

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(SEQ ID NO: 13)

ATGGCAGATAAAAACAGAACATTTAAACTTGTAGGTGCAGGATCTTCTAG  
CACACAAGAAAAAATTGAAAAGCCTGCTCTTTCGTTTATGCAAGATGCGTG  
GCGTCGCTTGAAAAAAAACAAATTAGCAGTAGTTTCACTCTATTTATTAGC  
20 TCTTTTACTTACTTTTTTCGTTAGCCTCAAATTTATTTGTAACTCAGAAGGAT  
GCTAATGGGTTTGATTTCGAAAAAAGTAACGACATATCGCAACTTACCACCT  
AAATTGAGTTCAAACCTTCCTTTTTTGGGAATGGTAGCATTAAATCCATCA

20

(SEQ ID NO: 14)

MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRLKKNKLAVVSLYLLA  
25 LLLTFLASNLFTVQKDANGFDSKKVTTYRNLPPKLSSNLPFWNGSINPS

25

Sequence description:

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A] Current length is 303 bp - 101 aa  
B] No obvious signal peptide but Shine Dalgarno sequence upstream of the ATG start codon. Not identified directly using the LEEP system but was found directly downstream of ID-34 described in WO 00/06736.

35

ID-83

Clone 98

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(SEQ ID NO: 15)

ATGAAAATAGTAGTACCAGTAATGCCTCGCAGTCTTGAAGAGGCTCAAGA  
AATAGATTTATCAAAATTTGATAGTGTTGATATTATTGAATGGCGAGCTGA



5 TGCCTTACCAAAGGATGACATTATTAATGTAGCTCCAGCTATTTTTGAGAA  
ATTCGCAGGTCATGAAATTATTTTTACTTTTCGTACAACGCGTGAAGGTGG  
TAATATTGTCTTATCTGATGCTGAGTATGTTGAGTTAATCCAGAAAATTAA  
TTCTATCTACAATCCAGATTATATTGATTTTGAGTATTTTTTCACATAAAGAA  
GTTTTTCAAGAAATGCTAGAATTTCCAAATTTAGTCCTGTCTTATCACAATT  
TTCAAGAGACACCGGAGAATATTATGGAGATATTTTCAGAATTAACAGCC  
CTAGCACCACGAGTTGTGAAAATCGCAGTAATGCCAAAGAATGAACAAGA  
TGTCTTAGACGTTATGAATTACACTCGCGGTTTCAAGACTATTAATCCTGA  
TCAAGTTTATGCGACGGTATCTATGAGTAAAATTGGACGTATTTCTCGTTTT  
10 GCTGGTGATGTAAGTGGATCTAGTTGGACATTTGCATATTTAGATTTCATCT  
ATCGCACCCGGACAAATTACTATTTTCAGAGATGAAGCGTGTCAAAGCATT  
GCTTGACGCTGACTGA

(SEQ ID NO: 16)  
15 MKIVVPVMPRSLEEAEIDLSKFDSVDIIIEWRADALPKDDIINVAPAI FEKFAG  
HEIIFTFRTTREGGNIVLSDAEYVELIQKINSIYNPDYIDFEYFSHKEVFQEMLEF  
PNLVLSYHNFQETPENIMEIFSELTALAPRVVKIAVMPKNEQDVLDVMNYTRG  
FKTINPDQVYATVSMISKIGRISRFAGDVTGSSWTFAYLDSSIAPGQITISEMKRV  
20 KALLDAD\*

Sequence description:

25 A] Length 678 bp, 225 aa (full length gene)  
B] No obvious signal peptide, but there is a  
Shine Dalgarno immediately upstream of ORF.

30 ID-84

Clone RS-52

(SEQ ID NO: 17)  
35 ATGAAAGACTTATTTGCAACAACAGAAGCATCATCAAGGAAACAGGAACA  
AGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAACAAATGGTA  
ATCAAATAAAAAAAATTGAGTTTATCGACTTTCAAAAAAATGAGATGACA  
GGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCGATTAGTTTT  
TCTGAAGATAGAATTGGTGGTAACTTAGAGCATTAGGATATCAACCGAA  
TGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCAAATGTTAATGA  
40 TATTGAAGTGATTTATATGAAGAAAGAATAG

(SEQ ID NO: 18)

MKDLFATTEASSRKQEQDRIVNYIKQHVELTNGNQIKKIEFIDFQKNEMTGTW  
GISTKINEQFSISFSEDRIGGKLRLALGYQPNEIGFSKDINSNNQNVNDIEVIYMK  
KE\*

5

Sequence description:

A] length: 333 bp - 111 aa (partial sequence)

10

B] No obvious Shine Dalgarno sequence upstream  
of the ATG start codon, and no obvious signal  
peptide within the protein.

ID-85

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Clone RS-53

(SEQ ID NO: 19)

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ATGAAAAAACGTATATGGTATTTGATAATAATAATCACAGTAATTTTAGGA  
GGACTAGCCATGAAAAACTTATTTGCAACAACAGAAGCATCATCAAGGAA  
ACAGGAACAAGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAA  
CAAATGGTAATCAAATAAAAAAAATTGAGTTTATCGACTTTCAAAAAAAT  
GAGATGACAGGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCG  
ATTAGTTTTTCTGAAGATAGAATTGGTGGTAAACTTAGAGCATTAGGATAT  
25 CAACCGAATGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCA

(SEQ ID NO: 20)

30

MKKRIWYLIHITVILGGLAMKNLFATTEASSRKQEQDRIVNYIKQHVELTNGN  
QIKKIEFIDFQKNEMTGTWGISTKINEQFSISFSEDRIGGKLRLALGYQPNEIGFSK  
DINSNNQ

Sequence description:

35

A] Length: 351 bp - 117 aa (Partial sequence)

B] Obvious signal peptide and Shine Dalgarno  
sequence upstream of the ATG start codon.

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ID-86

Clone ID-74

(SEQ ID NO: 21)

ATGTCAAATCAATATGATTATATCGTTATTGGTGGAGGTAGT  
GCAGGCAGTGGTACCGCTAATAGGGCAGCCATGTATGGAGC  
AAAAGTCCTGTTAATTGAAGGTGGACAAGTAGGTGGAACCTTG  
5 TGTAACTTAGGTTGTGTACCTAAGAAAATCATGTGGTATGG  
TGCACAAGTTTCTGAGACACTCCATAAGTATAGTTCAGGTTA  
TGGTTTTGAAGCCAATAATCTTAGTTTTGATTTTACTACTCTA  
AAAGCTAATCGCGATGCTTACGTGCAGCGGTCTAGACAGTCG  
TATGCCGCTAATTTTGAGCGTAATGGGGTCGAAAAGATTGAT  
10 GGATTTGCTCGTTTTATTGATAACCATACTATTGAAGTGAATG  
GTCAGCAATATAAAGCTCCTCACATTACTATTGCAACAGGTG  
GACACCCTCTTTACCCTGATATTATTGGAAGTGAACCTTGGTG  
AGACTTCTGATGATTTTTTTGGATGGGAGACCTTACCAAATTC  
TATATTGATTGTTGGGGCGGGCTATATCGCGGCAGAACTTGC  
15 TGGAGTGGTTAATGAATTAGGCGTTGAAACCCATCTTGCATT  
TAGAAAAGACCATATTCTACGCGGATTTGATGACATGGTAAC  
AAGTGAGGTTATGGCTGAAATGGAGAAATCAGGTATCTCTTT  
ACATGCTAACCATGTACCTAAATCTCTTAAACGCGATGAAGG  
TGGCAAGTTGATTTTTGAAGCTGAAAATGGGAAAACGCTTGT  
20 CGTTGATCGTGTAATATGGGCTATCGGCCGTGGACCAAATGT  
AGACATGGGACTTGAAAATACCGATATTGTTTTAAATGATAA  
AGATTATATCAAAACAGATGAATTTGAGAATACTTCTGTAGA  
TGGCGTGTATGCTATTGGAGATGTTAATGGGAAAATTGCCTT  
GACACCGGTAGCAATTGCAGCAGGTCGTTCGCTTATCAGAAAG  
25 ACTTTTTAATCATAAAGATAACGAAAAAATTAGATTACCATAA  
TGTACCTTCAGTTATTTTTACTCACCTGTAATTGGGACGGTA  
GGACTTTCAGAAGCAGCAGCTATCGAGCAATTTGGAAAAGAT  
AATATCAAAGTCTATACATCAACTTTTACCTCTATGTATACGG  
CTGTTACCAGTAATCGCCAAGCAGTTAAGATGAAGCTCATAA  
30 CCCTAGGAAAAGAGGAAAAAAGTTATTGGGCTTCATGGTGTTG  
GTTATGGTATTGATGAAATGATTCAAGGTTTTTCAGTTGCTAT  
CAAAATGGGGGCTACTAAAGCAGACTTTGATGATACTGTTGC  
TATTCACCCAACTGGATCTGAGGAATTTGTTACAATGCGCTA  
A

35

(SEQ ID NO: 22)

MSNQYDYIVIGGGSAGSGTANRAAMYGAKVLLIEGGQVGGTC  
VNLGCVPKKIMWYGAQVSETLHKYSSGYGFEANNLSFDFTTLK  
ANRDAYVQRSRQSYAANFERNGVEKIDGFARFIDNHTIEVNQ  
40 QYKAPHITATGGHPLYPDIIGSELGETSDDFFGWETLPNSILIVG  
AGYIAAELAGVVNELGVETHLAFRKDHILRGFDDMVTSEVMAE  
MEKSGISLHANHVPKSLKRDEGGKLIFEANGKTLVVDRVIWAI  
GRGPNVDMGLENTDIVLNDKDYIKTDEFENTSVDGVYAIGDVN  
GKIALTPVAIAAGRRLSERLFNHKDNEKLDYHNVPSVIFTHPVIG

TVGLSEAAAIEQFGKDNIKVYTSTFTSMYTAVTSNRQAVKMKLI  
TLGKEEKVIGLHGVGYGIDEMIQGFSSVAIKMGATKADFDDTVAI  
HPTGSEEFVTMR\*

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ID-87

Clone RS-55

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(SEQ ID NO: 23)

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ATGACAAAAAACATCTTAAAACGCTTGCCTTGGCACTTACTACAGTATCA  
GTAGTGACATACAGCCAGGAGGTATATGGATTAGAAAGAGAGGAATCGGT  
CAAACAAGAACAACCCAGTCAGCTTCAGAAGATGATTGGTTCTGAAGAAG  
ATAATGAGAGGAAAACAAATGTTTCTAAAGAGAATTCTACTGTTGATGAA  
ACAGTTAGTGATTTATTTTCTGATGGAAATAGTAATAACTCTAGTTCTAAA  
ACCGAGTCAGTGGTAAGTGACCCTAAACAAGTCCCCAAAGCAAAACCAGA  
GGTTACACAAGAAGCAAGCAATTCTAGTAATGATGCTAGCAAAGTAGAAG  
TACCAAAACAGGATACAGCTTCAAAAAAGGAAACTCTAGAAACATCAACT  
TGGGAGGCAAAAGATTTTCGTAAGTACTAGAGGGGATACTTTAGTAGGTTTTTCA  
AAATCTGGAATTAATAAGTTATCTCAAACATCACACTTGGTTTTTACCAAGT  
CATGCAGCAGATGGAAGTCAATTGACACAAGTAGCTAGCTTTGCTTTTACT  
CCAGATAAAAAGACGGCCATTGCAGAATATACAAGTAGGCTAGGAGAAA  
ATGGGAAACCGAGTCGTTTATAGATATTGATCAGAAGGAAATTATTGATGAG  
GGAGAAATATTTAATGCTTACCAGTTGACTAAGCTTACTATTCCAAATGGT  
TATAAGTCTATTGGTCAAGATGCTTTTGTGGACAATAAGAATATTGCTGAG  
GTTAACCTTCCTGAGAGTCTCGAGACTATTTTCAAGTATGCTTTTGTCTACA  
TGTCTTTTAAACAAGTAAAGTTACCAGATAACCTAAAGGTCATTGGAGAA  
TTAGCTTTTTTTTGATAATCAGATTGGTGGTAAGCTTTACTTGCCACGTCCT  
TGATAAAATTAGCAGAACGCGCTTTCAAATCTAATCGTATTCAAACAGTTG  
AATTTTTTGGGAAGTAAGCTTAAGGTTATAGGAGAAGCAAGTTTTCAAGAT  
AATAATCTGAGGAATGTTATGCTTCCGGATGGACTTGAAAAAATAGAATC  
AGAAGCTTTTACAGGAAATCCAGGAGATGAACATTACAACAATCAGGTTG  
TATTGCGCACAAGGACAGGCCAAAATCCACATCAACTTGCGACTGAGAAT  
ACTTACGTCAATCCGGACAAATCATTGTGGCGTGCAACACCTGATATGGAT  
TATACCAAATGGTTAGAGGAAGATTTTACCTATCAAAAAAATAGTGTTACA  
GGTTTTTTCAAATAAAGGCTTACAAAAGGTAAGACGTAATAAAAACTTAGA  
AATTCCAAAACAACACAATGGTATTACTATTACTGAAATTGGTGATAACGC  
TTTTCGCAATGTTGATTTTCAAAGTAAACTTTACGTAAATATGATTTGGA  
AGAAATAAAGCTCCCCCTCAACTATTCGGAAAATAGGTGCTTTTGTCTTTCA  
ATCTAATAACTTGAAATCCTTTGAAGCAAGTGAAGATTTAGAAGAGATTA  
AAGAGGGAGCCTTTATGAATAATCGTATTGGAAGTCTAGACTTGAAAGAC  
AACTTATCAAAATAGGTGATGCTGCTTTCCATATTAATCATATTTATGCC  
ATTGTTCTTCCAGAATCTGTACAAGAAATAGGACGTTTCAAGCTTTTCGACAA  
AATGGTGCGCTTCACCTTATGTTTATCGGAAATAAGGTTAAACAATTGGT

GAAATGGCTTTTTTATCCAATAAACTGGAAAGTGTAATCTCTCTGAGCAA  
AAACAATTAAAGACAATTGAGGTCCAAGCTTTTTTCGGATAATGCCCTTAGT  
GAAGTAGTCTTACCGCCAAATTTACAGACTATTCGTGAAGAGGCTTTCAAA  
AGGAATCATTTGAAAGAAGTGAAGGGTTCATCTACATTATCTCAGATTACT  
5 TTTAATGCTTTTGATCAAAATGATGGGGACAAACGCTTTGGTAAGAAAGTG  
GTTGTTAGGACACATAATAATTCTCATATGTTAGCAGATGGTGAGCGTTTT  
ATCATTGATCCAGATAAGCTATCTTCTACAATGGTAGACCTTGAAAAGGTT  
TTAAAAATAATCGAAGGTTTAGATTACTCTACATTACGTCAGACTACTCAA  
ACTCAGTTTAGAGAAATGACTACTGCAGGTAAAGCGTTGTTATCAAAATCT  
10 AACCTCCGACAAGGAGAAAAACAAAAATTCCTTCAAGAAGCACAATTTTT  
CCTTGGTCGCGTTGATTTGGATAAAGCCATAGCTAAAGCTGAGAAGGCTTT  
AGTGACCAAGAAGGCAACAAAGAATGGTCATTTGCTTGAGAGGAGTATTA  
ACAAAGCGGTATTAGCTTATAATAATAGTGCTATTAAAAAAGCTAATGTTA  
AGCGCTTGGA AAAAGAGTTAGACTTGCTGACAGATTTAGTCGAGGGGAAAA  
15 GGACCATTAGCGCAAGCTACAATGGTACAAGGAGTTTATTTATTAAAGAC  
GCCTTTACCATTGCCAGAATATTATATCGGATTGAACGTTTATTTTGACAA  
GTCTGGAAAATTGATTTATGCACTTGATATGAGTGATACTATTGGCGAGGG  
ACAAAAAGATGCATATGGTAATCCTATATTAAATGTTGACGAGGATAATG  
AAGGTTATCATACCTTGGCAGTTGCCACTTTAGCTGATTATGAAGGTCTTT  
20 ATATTAAAGATATTTTAAATAGTTCCCTTGATAAGATTAAAGCAATACGCC  
AGATTCCTTTGGCAAAATATCATAGATTAGGAATTTTCCAAGCTATCCGAA  
ATGCAGCGGCAGAAGCAGACCGATTGCTTCCTAAGACACCTAAGGGGTAC  
CTAAATGAAGTCCCAAATTATCGTAAAAAACAATGGAGAAAAATTTAAA  
ACCAGTTGATTATAAAACGCCGATTTTAAATAAGGCTTTACCTAATGAAAA  
25 GGTAGACGGTGATAGAGCGGCTAAAGGTCATAATATAAATGCGGAGACTA  
ATAATTCTGTAGCTGTAACACCAATAAGGTCCGAGCAGCAATTACATAAGT  
CACAGTCTGATGTAAATTTACCTCAAACAAGTTCTAAAAATAATTTTATAT  
ACGAGATTCTAGGATACGTTAGTTTATGTTTGCTTTTCCTAGTAACTGCTGG  
GAAAAAAGGAAAACGAGCAAGAAAATAA

30 (SEQ ID NO: 24)  
MTKKHLKTLALALTTVSVVTYSQEVYGLEREESVKQEQTQSASEDDWFEEDN  
ERKTNVSKENSTVDETVSDLFSDGNSNNSSSKTESVVSDPKQVPKAKPEVTQE  
ASNSSNDASKVEVPKQDTASKKETLETSTWEAKDFVTRGDTLVGFSKSGINKL  
35 SQTSHLVLP SHAADGTQLTQVASFAFTPDKKTALAEYTSRLGENGKPSRLDIDQ  
KEIIDEGEIFNAYQLTKLTIPNGYKSIGQDAFVDNKNIAEVNLPESLETISDYAF  
AHMSLKQVKLPDNLKVIGELAFFDNQIGGKLYLPRHLIKLAERAFKSNRIQTV  
EFLGSKLKVIGEASFQDNNLRNVMLPDGLEKIESEAF TGNPGDEHYNNQVVLR  
TRTGQNPHQLATENTYVNPDKSLWRATPDMDYTKWLEEDFTYQKNSVTGFS  
40 NKGLQKVR RNKNLEIPKQHNGITITEIGDNAFRNVDFQSKTLRKYDLEEIKLPS  
TIRKIGAF AFQSNNLKSFEASEDLEEIKEGAFMNNRIGTLDLKD KLIKIGDAAFH  
INHIYAIVLPESVQEIGRSAFRQNGALHLMFIGNKVKTIGEMAFLSNKLESVNL  
SEQKQLKTIEVQAFSDNALSEVVLPNLTQIREEAFKR NHLKEVKGSS TSLSQITF  
NAFDQNDGDKRFGKKVVVRTHNNSHMLADGERFIIDPKLSSTMVDLEKVL

5 KII EGLDYSTLRQTTQTQFREMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGR  
VDLDKAIKAEKALVTKKATKNHLLERSINKAVLAYNNSAIKKANVKRLEK  
ELDLLTDLVEGKGPLAQATMVQGVYLLKTPPLPEYYIGLNVYFDKSGKLIYA  
LDMSDTIGEGQKDAYGNPILNVDEDNEGYHTLA VATLADYEGLYIKDILNSSL  
DKIKAIRQIPLAKYHRLGIFQAIRNAAAEADRLLPKTPKGYLNEVPNYRKKQM  
EKNLKPVDYKTPIFNKALPNEKVDGDRAAKGHNINAETNNSVAVTPIRSEQQL  
HKSQSDVNLPQTSSKNNFIYEILGYVSLCLLFLVTAGKKGKRARK\*

10 Sequence description:

A] Length 3168 bp - 1056 aa (Partial sequence)  
B] Obvious signal peptide with Shine Dalgarno  
sequence upstream of the ATG start codon.

15

ID-88

20 Clone RS-56

(SEQ ID NO: 25)  
GCAGGATACATCATGCACAAGCACGAGGCTATCGTGTCATGCTGGGGTCA  
ACCCAGGAAGACATGTCGGCACAAGCTGAAGATTTCTTTACAGTCTGTACA  
25 CAATAAAGAGACGGGTAAGAGCGCTTTTAATGACAAAGAACGACTAGCAA  
TT

(SEQ ID NO: 26)  
AGYIMHKHEAIVSCWGQPRKTCRHKLKISLQSVHNKETGKSAFNDKERLAI  
30

Sequence description:

35 A] Length:153 bp - 51 aa (partial sequence)  
B] No signal peptide visible, insufficient  
sequence data to determine the presence of a  
Shine Dalgarno sequence.

40 ID-89

Clone RS-58

(SEQ ID NO: 27)

GTGTCATTTATGCAAAGAAAATCCTATTTAAAATCCATGAGTGTTCTTACT  
TTAACAGCTTGTCTTATATCAGGATATGTGGTTAAAGATATTGCTATGTTA  
CATGCAGTATCTGCCAGTGAGAAGAAAGCAAATAATGTCAGTCCGAGAGA  
5 AAATCTCTACAGGGCTGTCAATGATAATTGGCTAGCCAATACAAAACCTCA  
AACAAGGGCAGACTAGTGTTAATAGTTTTTCAGAAATTGAGGATAAATTA  
AAGCAACTGTTAGTGTCTGATATGGCTAAAATGGCCTCAGGAAAGATTGA  
AACAACCAATGATGAACAGAAAAAAATGGTTGCATACTATAAACAAGGTA  
TGGACTTTAAAACAAGAGATAAAAAATGGTCTCAAACCTCTAAAACCAGTT  
10 TTACAAAAACTTGAAGCAGTCTCTTCAATGAAAGACTTTCAAAGTTTGGCC  
CATGATTTTGTGATGAGTGGTTTTGTTTTACCATTTGGTTTGACTGTGGAAA  
CCAATGCTCGAGATAATAGCCAAAAGCAATTGGTGCTTCGTCAAGCACCC  
GCATTACTTGAATCACCTGACCAATATAAGAAGGGCAATAAAGAAGGTGA  
GGCTAAATTATCAGCTTACCGTACTTCAGCAATGGCTTTGCTTAAACAAGC  
15 TGGAAAAAGTAACATTGAAGATAGAAAACTAGTTAAACAAGCTATAGCAT  
TTGATAGACTCTTATCAGAAAAAACGCAAGTTGATCAAAGTAAAATCACA  
GCTGAAAGTGAGACAGCTGCGGGGCGATATAACCCTGAAAGTATGGAAAC  
GGTTCACAATTACGCCAAGGAATTTGACTTTAAAGAATTGATTGAAAAACT  
AGTTGGGCCAACGAATAAGGCAGTCAATGTAGAAGATAAACTTATTTTA  
20 AACAGGTTAATGATGTTATAAATAGTAAACAATTAGCCAATATGAAAGCA  
TGGATGATGATTTCTATGCTAGTTGATCAATCAGATTTTCTAGGAGAACAA  
AATCGTCAAGCAGCGAGTGCTTTTAAGAATGTTGCGTCTGGTTTGACTCAG  
ATTGAATCGAAAGAAAAAATGCTTACACCCAATTAG

25

(SEQ ID NO: 28)

MSFMQRKSYLKSM SVLT LTACLISGYVVKDIAM LHAV SASEKKANNVSPREN  
LYRA VNDNWLANTKLKQGQTSVNSFSEIEDKLKQLLVSDMAKMASGKIETTN  
DEQKKMVA YYKQGMDFKTRDKNGLKPLKPV LQKLEAVSSMKDFQSLAHDF  
30 VMSGFVLPFGLTVETNARDNSQKQLVLRQAPALLES PDQYKKGNKEGEAKLS  
AYRTS AMALLKQAGKSNIEDRKL VKQAIAFDRL LSEKTQVDQSKITAESETAA  
GRYNPESMETVHNYAKEFDFKELIEKLVGPTNKAVNVEDKTYFKQVNDVINS  
KQLANMKAWMMISMLVDQSDFLGEQNRQAASAFKNVASGLTQIESKEKMLT  
PN\*

35

Sequence description:

- 40 A] Length: 1095 bp - 365 aa (full-length gene)  
B] an GTG (possible ATG start codon located 7 bp  
further downstream) start codon with an obvious  
signal peptide. Shine Dalgarno sequence present  
upstream of the ORF.

ID-90

Clone RS-59

5

(SEQ ID NO: 29)

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTAAAATGAG  
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC  
CTACTTTTTATTTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC  
GTTATTTAAATATTTTTTATAG

10

(SEQ ID NO: 30)

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTVAVILSLFK  
YFL\*

15

Sequence description:

20

A] Length: 174 bp - 58 aa(full length gene)  
B] No obvious signal peptide, but Shine  
Dalgarno sequence is present upstream of ATG  
start codon.

25

ID-91

Clone RS-62 (partial sequence)

30

(SEQ ID NO: 31)

ATGCAGGTATTTTTAAATATTGTCAATAAATTCTTTGATCCAGTTATTCATA  
TGGGTTCGGGAGTTGTGATGCTAATTGTCATGACAGGTTTAGCCATGATAT  
TTGGAGTGAAGTTTTCTAAAGCACTTGAAGGTGGTAT

35

(SEQ ID NO: 32)

MQVFLNIVNKFFDPVIHMGSGVVMLIVMTGLAMIFGVKFSKALEGG

Sequence description:

40

A] Length: 141 bp - 41 aa (partial sequence  
B] Shine Dalgarno sequence present upstream of  
ATG start codon with a possible signal peptide  
present





ID-92

5 Clone RS-69 (partial sequence)

(SEQ ID NO: 33)

10 ATGAAAAAGAAAACATTCAGTGCTTATAACTTTTTAACGGCTCTTATCCTT  
TGCTTTTTGACAGTGCTTTTTATCTTTCCATTTTATTGGATTATGACAGGAG  
CTTTTAA

(SEQ ID NO: 34)

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAF

15

Sequence description:

20 A] Length: 110 bp -36 aa (Partial sequence)  
B] Possible signal peptide with Shine Dalgarno  
sequence directly upstream of the ATG start  
codon.

25 ID-93

Clone RS-70

(SEQ ID NO: 35)

30 ATGACTGAGAACTGGTTACATACTAAAGATGGTTCAGATATTTATTATCGT  
GTCGTTGGTCAAGGTCAACCGATTGTTTTTTTACATGGCAATAGCTTAAGT  
AGTCGCTATTTTGATAAGCAAATAGCATATTTTTCTAAGTATTACCAAGTT  
ATTGTTATGGATAGTAGAGGGCATGGCAAAGTCATGCAAAGCTAAATAC  
35 CATTAGTTTCAGGCAAATAGCAGTTGACTTAAAGGATATCTTAGTTCATTT  
AGAGATTGATAAAGTTATATTGGTAGGCCATAGCGATGGTGCTAATTTAGC  
TTTAGTTTTTCAAACGATGTTTCCAGATATGGTTAGAGGGCTTTTGCTTAAT  
TCAGGGAACCTGACTATTCATGGTCAGCGATGGTGGGATATTCTTTTAGTA  
AGGATTGCCTATAAATTCCTTCACTATTTAGGGAAACTCTTCCGTATATG  
40 AGGCAAAAAGCTCAAGTTAFTTCGCTTATGTTGGAGGATTTGAAGATTAGT  
CCAGCTGATTTACAGCATGTGTCAACTCCTGTAATGGTTTTGGTTGGAAAT  
AAGGACATAATTAAGTTAAATCATTCTAAGAACTTGCTTCTTATTTCCA  
AGGGGGGAGTTTTATTCTTTAGTTGGCTTTGGGCATCACATTATTAAGCAA  
GATTCCCATGTTTTTAATATTATTGCAAAAAGTTTATCAACGATACGTTG  
AAAGGAGAAATTGTTGAAAAAGCTAATTGA

(SEQ ID NO: 36)

MTENWLHTKDGSDIYYRVVGQGQPIVFLHGNSLSSRYFDKQIAYFSKYYQVIV  
MDSRGHGKSHAKLNTISFRQIAVDLKDILVHLEIDKVILVGHSDGANLALVFQ  
5 TMFPDMVRGLLLNSGNLTIHGQRWWDILLVRIAYKFLHYLGKLFYMRQKA  
QVISLMLEDLKISPADLQHVSTPVMVLVGNKDIKLNHSSKKLASYPFRGEFYSL  
VGFGHHIIKQDSHVFNIIAKKFINDTLKGEIVEKAN\*

10 Sequence description:

A] Length: 744 bp - 248 aa (full length gene)  
B] No obvious signal peptide, but Shine  
Dalgarno sequence upstream of the ATG start  
15 codon.

ID-94

20 Clone RS-71

(SEQ ID NO: 37)

ATGGTAGCAAAAGAGTTAGGTAAAAATAGCTTTACTATCCCAACTATTTGT  
TCTAATTGCTCCGCAGGTACTGCCATTGCAGTTGTATATAATGATGACCAT  
25 TCTTTCTTAAGATACGGCTATCCCGAGTCTCCACTTCATATTTTTATCAATA  
CACGGATCATTGCACAGGCACCAAGCAAATATTTTTGGGGCTGGTATTGGGG  
ACGGTATTTCAAAAGCCCCTGAAGTAGAACGTGCTACCTTAGAGGCTAAG  
ACCAATAAACTACCACATACTGCAGTGTTAGGACAAGCAGTCGCTCTGTCT  
TCAAAGGAAGCTTTTTATCAATTTGGTGAACAAGGTCTAAAAGACGTTGAA  
30 GCTAATTTAGCTTCGCGTGCAGTTGAAGAAATTGCGCTTGATATCTTA

(SEQ ID NO: 38)

MVAKELGKNSFTIPTICSNCSAGTAIAVVYNDDHSFLRYGYPEsplhifINTRIIA  
QAPSKYFWAGIGDGIKAPEVERATLEAKTNKLPHTAVLGQAVALSSEAFY  
35 QFGEQGLKDVEANLASRAVEEIALDIL

Sequence description:

40 A] Length: 405 bp - 135 aa (Partial sequence)  
B] No obvious Shine Dalgarno sequence upstream  
of the ATG start codon, probable signal  
peptide present at the N-terminus.

ID-95

Clone RS-73

5 (SEQ ID NO: 39)  
TTGAGGGAAACTTACTGGAAAATTTCAAGCGATTGCGATAAAATAAATCTT  
GCAGAGTTTTCTAGAGAAAGGAGGTCAGATTTATTGGAGTGGCAAGATCT  
AGCGCAGTTACCTGTATCTATTTTTTAAAGACTATGTTACAGATGCTCAAGA  
CGCGGAAAAAACCTTTTATATGGACAGAAGTATTTTAAAGGGAGATTAATCG  
10 CTCAAATCAAGAAATTATTTTGCATATTTGGCCGATGACTAAGACAGTCAT  
TCTGGGGATGTTAGATCGAGAATTACCACATTTAGAATTAGCTAAAAAAG  
AAATCATCAGTCGTGGTTATGAACCAGTTGTTTCGGAATTTTGGAGGTCTCG  
CAGTTGTAGCTGATGAAGGAATTTTAAATTTTTCATTGGTTATTCCAGATGT  
TTTTGAGAGAAAATTGTCTATCTCAGATGGGTATCTTATAATGGTCGATTTT  
15 ATTAGAAGTATATTTTCGGATTTTATCAACCTATTGAGCACTTTGAAGTA  
GAGACCTCCTATTGTCCTGGTAAGTTTGATCTTAGTATAAATGGCAAAAAA  
TTTGCTGGCTTGGCTCAGCGCCGTATAAAGAATGGTATTGCGGTATCAATT  
TACCTTAGCGTTTGTGGCGATCAAAAAGGGCGGAGTCAAATGATTTTCAGAT  
TTTTATAAGATTGGTCTAGGTGATACGGGTAGTCCAATTGCTTATCCAAAT  
20 GTAGATCCTGAAATTATGGCTAATCTATCTGATCTATTAGATTGTCCTATG  
ACAGTAGAAGATGTTATTGATCGTATGTTGATTAGCCTTAAACAAGTAGGT  
TTTAATGATCGTTTACTGATGATTAGACCCGATTTAGTTGCAGAGTTTGAT  
AGATTTTCAGGCTAAGTCTATGGCTAATAAGGGGATGGTGAGCAGAGATGA  
ATAA

25 (SEQ ID NO: 40)  
MRETYWKISSDCDKINLAEFSRERRSDLLEWQDLAQLPVSIFKDYVTDAQDAE  
KPFIWTEVFLREINRSNQEIILHIWPMKTVILGMLDRELPHLELAKKEIISRGYE  
PVVRNFGGLAVVADEGILNFSLVIPDVFERKLSISDGYLMVDFIRSIFSDFYQPI  
30 EHFEVETSYCPGKFDLSINGKKFAGLAQRRIKNGIAVSIYLSVCGDQKGRSQMI  
SDFYKIGLGD TGSP IAYPNVDPEIMANLSDLLDCPMTVEDVIDRMLISLKQVGF  
NDRLLMIRPDLVAEFDRFQAKSMANKGMVSRDE\*

35 Sequence description:

40 A] Length: 921 bp -307 aa (Full-length gene sequence)  
B] No obvious Shine Dalgarno sequence upstream  
of the TTG start codon or signal peptide  
visible. Actual start point may be a further  
85 bp downstream (TTG). This start point is  
preceded by a typical Shine-Dalgarno sequence.

ID-96

Clone RS-74

5

(SEQ ID NO: 41)

TTGGAAGGTTTACTTATTGCATTGATTCCCATGTTTGCCTGGGAAAAGTATT  
GGATTTGTTAGTAATAAAAATTGGAGGGCGTCCAAATCAACAAACATTTGG  
AATGACTTTAGGAGCATTGCTATTTGCGATTATCGTATGGTTATTTAAACA  
10 GCCAGAGATGACTGCCTCATTGTGGATTTTGGTATCTTAGGTGGTATCCT  
ATGGTCAGTCGGCCAAAATGGTCAATTTCAAGCAATGAAATATATGGGAG  
TCTCTGTTGCTAATCCACTGTCAAGTGGTGCACAATTAGTAGGTGGAAGCC  
TAGTTGGTGCTTTAGTCTTTCATGAATGGACTAAGCCAATCCAATTTATTTT  
AGGATTGACAGCGTTGACATTATTAGTTATCGGCTTCTATTTCTCAAGTAA  
15 ACGTGATGTTTCAGAACAAGCTTTGGCAACACATCAAGAGTTTTCAAAAAG  
GATTTGCTACAATTGCTTATTCAACTGTAGGTACATCTCGTACGCAGTTTT  
ATTTAACAACATTATGAAGTTCGACGCTATGGCCGTCATTTTACCCATGGC  
TGTTGGAATGTGTCTAGGTGCAATTTGTTTCATGAAGTTTCGTGTAACTTT  
GAGGCTGTTGTTGTTAAAAATATGATTACAGGTCTCATGTGGGGCGTTGGT  
20 AATGTCTTCATGTTATTGGCAGCAGCTAAAGCAGGGCTAGCAATTGCTTTT  
AGTTTTTCTCAACTTGGAGTAATTATCTCTATTATTGGTGGTATTTTATTTT  
AGGTGAGACAAAAACGAAGAAAGAGCAGAAATGGGTGTTCATGGGTATC  
CTTTGTTTTGTTATGGGTGCTATATTACTTGGTATTGTAAATCTTATTAA

25

(SEQ ID NO: 42)

MEGLLIALIPMFAWESIGFVSNKIGGRPNQQTFGMTLGALLFAIIVWLFKQPEM  
TASLWIFGILGGILWSVGQNGQFQAMKYMGVSVANPLSSGAQLVGGSLVGAL  
VFHEWTKPIQFILGLTALTLLVIGFYFSSKRDVSEQALATHQEFSKGFATIAYST  
VGYISYAVLFNNIMKFDAMAVILPMAVGMCLGAICFMKFRVNFEAVVVKNMI  
30 TGLMWGVGNVFMLLAAAKAGLAIAFSFSQLGVIISIIGGILFLGETKTKKEQK  
WVVMGILCFVMGAILLGIVKSY\*

35 Sequence description:

A] Length: 867 bp - 289 aa (full-length gene)  
B] Possible Shine Dalgarno sequence upstream of  
GTG start codon, no obvious signal peptide  
present.

40

ID-97

Clone RS-75

(SEQ ID NO: 43)

5 ATGACAACTTACTACGAAGCTATAAACTGGAACGAAATTGAAGATGTTAT  
TGATAAATCAACTTGGGAAAACTAACCGAACAATTTTGGCTCGATACAC  
GTATCCCTTTATCAAATGACTTAGACGATTGGCGCAAACCTTCCGCTCAAG  
AAAAAGATCTTGTTGGCAAGGTTTTTGGAGGCTTAACCCTACTTGATACCA  
TGCAATCAGAACTGGTGTTGAAGCTATTCGTGCCGATGTTTCGCACGCCTC  
ACGAAGAAGCTGTCTTAAACAATATTCAATTCATGGAATCTGTTACGCTA  
AATCTTATTCTTCAATTTTCTCAACTTTAAATACTAAATCAGAAATTGAAG  
10 AAATTTTTCGAGTGGACTAATAATAATGAGTTCCTTCAAGAAAAAGCACGT  
ATTATCAATGACATTTATGCTAATGGAAATGCCCTTCAAAAAAGGTGGCT  
TCCACCTACCTCGAACTTTCCTTTTTTATTCTGGCTTTTTCACACCTCTTTA  
CTATTTGGGAAATAATAAGTTAGCAAATGTTGCTGAAATCATTAATAAT  
TATTCGTGATGAATCTGTACATGGTACTTATATCGGTTACAAATTCCAGCTT  
15 GGTTTTAACGAATTACCAGAAGATGAGCAAGAGAATTTTCGTGATTGGAT  
GTATGACCTCCTTTATCAGCTGTATGAAAACGAAGAAAAATACACCAAGA  
CACTTTATGATGGCGTAGGATGGACTGAAGAAGTTATGACCTTTTTACGCT  
ACAATGCTAATAAAGCTCTTATGAATTTAGGACAAGATCCTTTATTCCCAG  
ATACAGCAAATGATGTCAACCCAATTGTTATGAATGGTATTTCAACAGGAA  
20 CATCAAACCATGACTTCTTCTCTCAAGTAGGTAATGGTTACCTACTTGGTA  
GCGTTGAAGCTATGCATGATGATGACTATAACTATGGATTATAA

(SEQ ID NO: 44)

25 MTTYEAINWNEIEDVIDKSTWEKLTEQFWLDTRIPLSNDLDDWRKLSAQEK  
DLVGKVFGGLTLLDTMQSETGVEAIRADV RTPHEEAVLNNIQFMESVHAKSY  
SSIFSTLNTKSEIEEIFEWTNNNEFLQEKARIINDIYANGNALQKKVASTYLETF  
LFYSGFFTPLYLGNKLANVAEIIKLIIRDESVHGTYIGYKFQLGFNELPEDEQ  
ENFRDWMYDLLYQLYENEEKYTKTLYDGVGWTEEVMTFLRYNANKALMNL  
30 GQDPLFPDTANDVNPIVMNGISTGTSNHDFFSQVGNGYLLGSVEAMHDDYN  
YGL\*

Sequence description:

35 A] Length: 960 bp - 320 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, but no signal peptide  
present.

40

ID-98

Clone RS-77 (partial sequence)

(SEQ ID NO: 45)

ATGAATTGGTCACGTATCTGGGAACTCGTAAAAATTAATATCCTTTATTCA  
AACCCCTCAGACTCTATCGGCACTAAGAAAAAAGCAAGAAAAGCATCCTAA  
AAAAGAATTTTCAGCTTATAAATCCATGTTTAGAAATCAGTTATTTTCAGAT  
TTTGCTCTTTTCAATAATTTATGTATTTCTCTTTGTATCACTTGATTTTAAAG  
AATATCCGGGCTATTTACAGTTCTACATTGGTATCTTTACACTAGTATCCAT  
TATCTACTCTTTTATTGCGATGTACAGTGTCTTCTATGAGAGTGACGATGTT  
AA

(SEQ ID NO: 46)

MNWSRIWELVKINILYSNPQTLSALRKKQEKHPKKEFSAYKSMFRNQLFQILL  
FSIIYVFLFVSLDFKEYPGYFTFYIGIFTLVSIYSFIAMYSVFYESDDV

Sequence description:

A] Length: 311 bp - 103 aa (Partial sequence)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, no obvious signal peptide at  
N-terminus.

ID-99

Clone RS-78 (partial sequence)

(SEQ ID NO: 47)

TAATCTTTTAGTCAACGGAGCAACAGGAAAATTGCAGGCTATGCGACAGA  
TATTCCACCACATAATTTAGCAGAAGTCATTGATGCTGTCGTGTACATGAT  
TGATCACCCTAAAGCTAAATTAGATAAATTAATGGAATTTCTACCTGGTCC  
AGATTTTCCAACCTGGCGCTATCATTCAAGGAAAAGATGAAATTCGTAAGG  
CATATGAGACTGGTAAGGGGAGAGTAGCGGTTTCGCTCGCGAACTGCTATT  
GAAACCTTAAAAGGTGGTAAGAAACAAATTATTGTTACTGAAATTCCTTAT  
GAAGTTAAT

(SEQ ID NO: 48)

SFSQRSNRKIAGYATDIPPHNLAEVIDAVVYMHDPKAKLDKLMFLPGPDFPT  
GAIQKGKDEIRKAYETGKGRVAVRSRTAIETLKGGKKQIIVTEIPYEVN

Sequence description:

A] Length: 312 bp - 104 aa (Partial sequence)  
B] No obvious Shine Dalgarno sequence or a

signal peptide. Both N- and C- termini of ORF  
yet to be elucidated.

5 ID-100

Clone RS-79

(SEQ ID NO: 49)

10 ATGGGACGTAAGTGGGCCAATATTGTTGCCAAAAAGACTGCTAAAGATGG  
TGCTAACTCAAAAGTATACGCTAAATTCGGTGTGAAATATATGTTGCTGC  
AAAGCAAGGTGAACCCAGACCCCGAGTCAAACCTCAGCTCTAAAATTCGTTT  
TGGACCGTGCTAAGCAAGCACAAAGTTCCAAAGCATGTTATTGATAAAGCG  
15 ATTGATAAAGCCAAAGGAAACACAGATGAAACTTTTCGTAGAGGGACGCTA  
TGAAGGTTTTGGTCCAAATGGTTCAATGATTATTGTGGATACTTTGACATC  
AAATGTTAACCGTACGGCAGCAAATGTACGTACTGCTTACGGTAAGAACG  
GTGGCAATATGGGAGCTTCAGGATCGGTATCCTACTTATTTGATAAAAAAG  
GTGTCATCGTTTTTGTCTGGTGATGATGCTGACACTGTCTTCGAACAATTACT  
20 TGAAGCGGATGTAGACGTAGATGATGTTGAAGCAGAAGAGGGAACAATA  
ACAGTTTATACCGCCCCAACAGATCTTCATAAAGGTATCCAAGCACTTCGC  
GATAATGGTGTAGAAGAATTCCAAGTTACTGAACTTGAAATGATTCCTCAA  
TCAGAAGTAGTATTGGAAGGTGATGACCTTGAACTTTTGAAAAGCTT

(SEQ ID NO: 50)

25 MGRKWANIVAKKTAKDGANSKVYAKFGVEIYVAAKQGEPPESNSALKFVL  
DRAKQAQVPKHVIDKAIDKAKGNTDETFVEGRYEGFGPNGSMIIVDTLTSNV  
NRTAANVRTAYGKNNGNMGASGSVSYLFDKKGIVVFAGDDADTVFEQLLEA  
DVDVDDVEAEEGTITVYTAPDLHKG IQALRDNGVEEFQVTELEMIPQSEVVL  
EGDDLETFEKL

30

Sequence description:

35 A] Length: 654 bp - 218 aa (Partial sequence)  
B] Possible Shine Dalgarno sequence upstream  
of ATG start, no obvious signal peptide

40 ID-101

Clone RS-80

(SEQ ID NO: 51)

TTGGAGAAATATTTGAAGAACCCGATTACATGGATTGGATTAGTTCTTGTG  
GTTACGTGGTTTTTAACTAAAAGTAGTGAATTTTTGATTTTTGGTGTGTGTG  
TCTTGTGTAGTATTTGCTAGTCAAAGTGAT

5

(SEQ ID NO: 52)

MEKYLKNPITWIGLVLVVTWFLTKSSEFLIFGVCVLLLVFASQSD

10 Sequence description:

A] Length: 135 bp - 45 aa (partial sequence)

B] Shine Dalgarno sequence upstream of TTG  
start codon with possible signal peptide

15

evident at N-terminus.

ID-102

20

Clone RS-81

(SEQ ID NO: 53)

ATGACACAATCAGATGCATATCTCTCGTTGAACGCGAAGACACGCTTTAGA  
GATCGCACAGGTAATTATCATTTTACTTCGGATAAAGAGGCTGTTGAACAA  
TATATGATAGAACATGTTGAACCTAATACGATGGTGTTCACATCACTAATT  
GAAAAGCTAGATTATTTGGTTTCTAATAACTACTATGAATCGGACCTTCTA  
AAACAATATAACCTTGAGTTTATTTGCCAAATTTTTGAGCATGCATACGCT  
AAGAAATTTGCTTTTCTAAATTTTATGGGGGCTTTAAAATTTTATAATGCTT  
ATGCTCTTAAT

25

30

(SEQ ID NO: 54)

MTQSDAYLSLNAKTRFRDRTGNYHFTSDKEAVEQYMIEHVEPNTMVFTSLIE  
KLDYLVSNYYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGALKFYNAYA  
LN

35

Sequence description:

40

A] Length: 318 bp - 106 aa (Partial sequence)

B] Shine Dalgarno sequence present upstream of  
ATG start codon, no obvious signal peptide



ID-103

Clone 2-11A

5 (SEQ ID NO: 55)  
ATGGTATTTATGGCAAATAAGAAAAAACAAGGAAAGAAAACCAGAA  
GACCTACTAAGGCAGAAATAGAGCGTCAAAGAGCTATTCAAAGGATGATT  
ACTGCTCTTGTTTTAACAATTATTCTCTTCTTTGGTATTATCAGATTAGGTA  
TTTTTGGTATTACAGTCTATAACGTCATCCGTTTTATGGTAGGTAGCTTGGC  
10 TTACTTATTTATTGCGGCAACTTTAATCTACCTTTATTTCTTTAAATGGTTG  
CGAAAGAAAGATAGCTTAGTAGCAGGTTTTTTGATAGCTTCTTTAGGATTA  
TTGATTGAGTGGCATGCTTACCTTTTCTCAATGCCTATTTTGAAAGATAAA  
GAAATTTTGCGTTCAACTGCTCGATTAATTGTGTCTGATTTAATGCAATTTA  
AAATCACTGTTTTTGCCGGTGGAGGTATGTTGGGTGCTTTGATTTACAAGC  
15 CAATTGCTTTTCTCTTTTCTAATATTGGTGCCTATATGATTGGTGTCTCTTC  
ATCATTTTGGGTCTCTTTTAAATGAGTTCTCTGGAAGTTTATGACATCGTCG  
AATTTATTAGAGCTTTTAAAAATAAAGTGGCAGAGAAGCACGAGCAAAAT  
AAAAAGGAGCGTTTTGCTAAGCGAGAGATGAAAAAAGCAATCGCTGAACA  
AGAGCGCATAGAGCGTCAAAAAGCTGAAGAAGAAGCTTATTTAGCTTCGG  
20 TTAATGTAGACCCTGAAACGGGTGAGATTCTAGAGGATCAAGCTGAGGAC  
AATTTGGATGATGCGCTACCACCTGAGGTAAGTGAAACATCAACTCCGGT  
ATTTGAGCCAGAGATCCTTGCTTATGAGACATCGCCTCAAAATGATCCTTT  
ACCAGTAGAGCCGACAATTTATTTAGAAGACTATGATTCCGCCGATTCCCTAA  
TATGAGAGAAAATGATGAGGAAATGGTTTATGATTTAGATGATGATGTAG  
25 ATGATAGTGATATAGAAAATGTCTGACTTTACACCTAAAACGACACTGGTTT  
ATAAATTACCAACGATAGATTTATTTGCACCAGATAAGCCTAAAAATCAAT  
CCAAAGAAAAGGATTTAGTCCGAAAGAATATCAGAGTTTTAGAAAGAAACA  
TTTAGAAGTTTTGGTATCGATGTAAAAGTAGAACGTGCTGAAATTGGACCA  
TCAGTTACTAAATATGAAATTAAACCAGCAGTTGGAGTTCGTGTGAATCGT  
30 ATTTCAAATCTATCTGACGACCTAGCTCTTGCTCTTGCAGCAAAAGATGTG  
CGTATAGAAGCACCAATTCCTGGAAAATCATTAAATAGGTATTGAAGTTCCT  
AACTCAGAAATTGCAACGGTTTTCTTTCCGCGAACTTTGGGAACAATCTGAT  
GCCAATCCTGAAAACCTTTTAGAAGTACCACTAGGAAAAGCTGTTAACGG  
CAATGCTCGCAGTTTTAACTTAGCTAGAATGCCGCATCTTTTGGTAGCTGG  
35 TTCAACTGGTTCAGGTAAATCTGTGGCAGTTAATGGAATTATTTCAAGTAT  
TTTGATGAAGGCACGTCCAGATCAAGTTAAGTTTATGATGATTGATCCCAA  
AATGGTTGAATTATCTGTTTATAATGATATTCCACATTTATTAATCCCTGTT  
GTAACCAATCCGCGTAAAGCAAGTAAGGCACTCCAAAAAGTTGTTGATGA  
AATGGAAAATCGATACGAGTTATTTAGCAAAATTGGTGTGCGTAATATAG  
40 CAGGTTATAATACAAAGGTTGAAGAGTTTAATGCTTCCTCTGAGCAAAAAC  
AAATGCCTTTGCCTTTAATCGTTGTCATTGTAGATGAATTGGCTGACTTGAT  
GATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATTCGTTTGGGGCAAAA  
AGCACGTGCTGCAGGTATCCATATGATTCTTGCAACTCAACGTCCATCCGT  
AGATGTTATTTCTGGTTTGATTAAAGCAAATGTTCCGTCGCGTATTGCATTT

5 GCTGTTTCAAGTGGTACTGATAGCCGTACGATCCTTGATGAAAATGGTGCT  
GAAAAGCTCTTGGGACGGGGTGACATGCTCTTTAAGCCTATTGATGAGAAT  
CATCCAGTACGACTACAAGGTTCTTTATTTTCAGATGATGATGTTGAAAGG  
ATCGTTGGTTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTTT  
10 GATCCTGGAGAAGTATCTGAAACAGATAACGGCTCTGGTGGTGGCGGCGG  
AGTACCTGAAAGTGATCCTCTTTTTGAAGAAGCCAAGGGACTCGTTTTAGA  
GACGCAAAAAGCAAGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTTT  
CAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTG  
GTCCAGCAGAAGGAACCAAGCCACGAAAAGTTTTAATGACTCCAACCTCCG  
AGTGAATAA

(SEQ ID NO: 56)  
15 MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIIFFGIIRLGIFGIT  
VYNVIRFMVGSLAYLFIAATLIYLYFFKWLRKKDSL VAGFLIASLGLLIEWHA  
YLFSMPILKDKEILRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIG  
AYMIGVLFILGLFLMSSLEVYDIVEFIRAFKNKVAEKHEQNKKERFAKREMK  
KAIAEQERIERQKAEEEEAYLASVNVDPETGEILEDQAEDNLDDALPPEVSETST  
20 PVFEPEILAYETSPQNDPLPVEPTIYLEDYDSPINMRENDEEMVYDLDDD VDD  
SDIENVDFTPKTTLVYKLPTIDLFAPDKPKNQSKEKDLVRKNIRVLEETFRSFGI  
DVKVERAEIGPSVTKEYEIKPAVGVRVNRISNLSDDLALALAAKDVRIEAPIPGK  
SLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPH  
LLVAGSTGSGKSVAVNGIISILMKARPDQVKFMMIDPKMVELSVYNDIPHLLI  
PVVTNPRKASKALQKVVDENRYELFSKIGVRNIAGYNTKVEEFNASSEQK  
25 QMPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVD  
VISGLIKANVPSRIAFVSSGTD SRTILDENGAEKLLGRGDMLFKPIDENHPVRL  
QGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGGVPESDPL  
FEEAKGLVLETQKASASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRK  
VLMTPTPSE\*

30 Sequence description:

35 A] Length: 2451 bp - 817 aa (Full-length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

40 ID-104

Clone 2-18/22b

(SEQ ID NO: 57)

ATGTCACAAGAGCAAGGAAAAATTTATATTGTAGAAGATGATATGACGAT  
TGTGTCACTTTTAAAAGATCATTTATCAGCTAGCTATCATGTCTCTAGTGTC  
AGCAATTTTCGTGATGTGAAACAAGAAATTATCGCATTTCAACCCGATTTG  
5 AACTAATGGATATTACGTTACCCTATTTTAATGGTTTTTACTGGACTGCAG  
AATTGCGTAAGTTTTTAACAATTCCTATTATTTTCATTTTCATCTAGTAATGA  
TGAAATGGATATGGTTATGGCATTAAATATGGGGGGTGATGACTTTATTTC  
AAAACCATTCTCTCTAGCTGTATTAGATGCTAAGCTAACTGCTATTTTAAG  
GAGAAGTCAACAATTTATCCAACAGGAATTAACTTTTGGGGGATTTACGTT  
GACAAGAGAAGGGTTATTGTCTAGCCAAGATAAAGAGGTTATTTTATCGC  
10 CAACAGAAAATAAAATCCTATCTATCTTGCTCATGCATCCTAAACAAGTAG  
TCTCAAAAGAGTCTCTATTAGAGAACTTTGGGAAAATGATAGTTTTATTG  
ATCAAAATACACTTAATGTTAATATGACACGCTTACGTAAAAAAATTGTCC  
CAATAGGTTTTGATTACATTCATACAGTGAGAGGAGTTGGGTATTTACTAC  
AATGA

15 (SEQ ID NO: 58)  
MSQEQGKIYIVEDDMTIVSLLKDHLASYSYHVSSVSNFRDVKQEIIAFQPDILM  
DITLPYFNGFYWTAELRKFLTPIIFISSNDEMMDVMALNMGGDDFISKPFSLA  
VLDAKLTAILRRSQQFIQQELTFGGFTLTREGLLSSQDKEVILSPTENKILSILLM  
20 HPKQVVSKESSLLEKLWENDSFIDQNTLVNMTRLRKKIVPIGFDYIHTVRGVG  
YLLQ\*

25 Sequence description:

A] Length: 669 bp - 223 aa (full-length gene  
sequence)  
B] Shine Dalgarno sequence present upstream of a GTG start codon.  
Was not identified directly by LEEP. This gene was found upstream of  
30 gene ID-10 described in WO 00/06736.

ID-105

35 Clone 2-20

(SEQ ID NO: 59)  
ATGTATCAAACCTCAGACAAATAAGGAAAAATTTGTTTTATTTTTGAAATTA  
TTTATCCCAGTATTGATTTATCAATTTGCTAATTTTTCAGCTACTTTTATTGA  
40 TTCGGTTATGACTGGACAGTATAGTCAGCTACATTTGGCAGGTGTGTCAAC  
TGCTAGTAATTTATGGAAGTCCGTTTTTCGCTTTATTAGTAGGTATGATTTCA  
GCATTAGTACCAGTAGTTGGTCAACATTTGGGTAGAGGAAATAAAGAACA  
AATTTCGCACAGAATTTTCATCAATTTCTATATTTAGGTTTGATACTGTCCTTA  
ATATTATTTTAAATCATGCAATTTATTGCTCAACCTGTCTTGGGGAGTTTGG

5 GTTTAGAAGATGAAGTTCTAGCAGTTGGTCGTGGTTATTTAAATTATATGT  
TGATTGGAATCATGCCGCTGGTGTGTTTAGCATTTGCCGTTCAATTCTTTGA  
TGCATTGGGGTTAACAAGGTTATCTATGTATCTGATGCTTTTAATTCTACCC  
TTTAATTCATTTTTTTAATTATATGCTTATCTACGGTAAATTTGGTATGCCTA  
10 GACTAGGAGGTGCGGGGGCAGGTCTTGGAACCTCTTTAACTTATTGGGCTA  
TTTTTATTGGTATTATTATTGTGATGTCACCTTCATCCTCAAATTAACATA  
TCATATATGGACTCTGGAAAGAATAAAAGCTCCTTTGATTATTGAAGATAT  
TCGATTGGGATTACCGATTGGTTTACAAATTTTTGCAGAAGTTGCAATTTTT  
GCAGTAGTAGGCTTATTCATGGCAAATTTTCTTCAATCATTATTGCAGCA  
15 CATCAGGCTGCTATGAATTTTTCATCATTAAATGTATGCATTTCTTTAAGTA  
TTTCCACTGCTCTAGCTATTACAATATCGTTTGAAGTAGGGGCAGAGCGCT  
TTCAGGACGCAACCACTTATAGTAGGATAGGACGCTTAACAGCGGTAGGG  
ATTACATCAGGAACCTTACTATTTTTATTTCTATTTTCGTGAGAATGTAGCAG  
CAATGTATAATAGTGCCCCTCACTTTGTGCTATTACAGCTCAATTCCTAAC  
20 TTATAGTCTCTTTTTCCAGTTTGCAGATGCTTATGCAGCTCCTGTACAGGGG  
ATTTTACGAGGCTATAAGGATACAACAAAACCATTTATGATCGGTGCGGG  
CTCTTATTGGTTATGTGCTTTGCCATTAGCGGTTATCTTAGAAAAAATAG  
CCAGTTAGGTCCGTTTGCCTATTGGATTGGTTTAATCACAGGTATTTTTGTT  
TGTGGTCTATTTCTAAACCAACGTCTGCAAAGATTAAGAAGTTGTATTAT  
TAA

(SEQ ID NO: 60)  
25 MYQTQTNKEKFVFLKLFIPVLIYQFANFSATFIDSVMTGQYSQLHLAGVSTAS  
NLWTPPFALLVGMISALVPVVGQHLGRGNKEQIRTEFHQFLYLGLLSLILFLI  
MQFIAQPVLGSLGLEDEVLA VGRGYLNYMLIGIMPLVLFSICRSFFDALGLTRL  
SMYLMLLILPFNSFFNYMLIYGKFGMPRLGGAGAGLGTSLTYWAIFIGIIIVMS  
LHPQIKTYHIWTLERIKAPLIHEDIRLGLPIGLQIFAEVAIFAVVGLFMAKFSSIIA  
AHQAAMNFSSLMYAFPLSISTALAITISFEVGAERFQDATTYSRIGRLTAVGITS  
30 GTLLFLFLFRENVAAAMYN SAPHFVAITAQFLTYSLFFQFADAYAAPVQGILRG  
YKDTTKPFMIGAGSYWLCALPLAVILEKNSQLGPFAYWIGLITGIFVCGLFLNQ  
RLQKIKKLYY\*

35 Sequence description:

A) Length: 1341 bp - 447 aa (full length gene)  
B) Shine-Dalgarno sequence present upstream of  
ATG start codon, There is a potential signal  
40 peptide sequence

ID-106

Clone 2-4A

(SEQ ID NO: 61)

5 TTGCTAGTTTCTTCTCTAGTTTCTTGTTTCATTTTTTCTTGTCATTTCGTCGTT  
GTCTTCATCAACACGAAATAAGTCTATAAACTTATCAAATAATTTTCATAGA  
CTTATTATATCAATTTTCAATAAAATGCTATAATAAAACCATGTCATTTTCA  
TTAAAAATTAGAAATCCATACGGTGAACATACCGTTAAAGAACTCCTTGA  
AGATTATTTTTTTGATTCCACGTAAGATTAGACATTTTTTTGCGTGTTAAAAAA  
CATGTACTTATAAACAATGAATTCATTAATTGGCAAACCTGTCGTCCAAGAA  
10 AACGATACTATTACCTTAATCTTTGATGATGAGGATTACCCTACTAAAAAA  
ATTCCTCTGGGCAGAGCAGAGCTTATTGATTGTCTTTATGAGGATGAACAT  
CTTATTATCGTTAATAAACCTGAAGGTATGAAAACCTCACGGTAACCAACCA  
AATGAAATAGCACTGTAAATCATGTATCTGCCTATTCTGGACAAACATGC  
TATGTTGTTTCATCGCCTAGATATGGAGACCAGTGGAGCTGTTTTATTTGCT  
15 AAAAATCCATTTATACTTCCCCTTATCAATCAACGCTTAGAACGAAAAGAA  
ATTTGGCGTGAATATTGGGCTTTAGTTGAAGGAAAATTTTCACCTAAGCAT  
CAAGTTTTTGAGAGACAAAATTGGACGGAACCGTCATGACAGACGTAAACG  
AATCATTGATTCTAAAAACGGTCAACATGCTATGACAATCATTGACGTTTT  
GAAGTATATCCAAAATAGTAGTCTCATAAAATGCCGACTGGAAACCGGAA  
20 GAACCCATCAAATTCGCATTCACTTATCTCATCACGGACATCCTTTAATAG  
GAGATCCCCTCTACAACCCTTCTTCTAATAATGAAAGGTTAATGCTACACG  
CTCACCGATTGACTCTATCCCATCCATTAACCTTGCGAAACTATTAGCGTAG  
AGGCCCTTCATCTACTTTTCGAGAAGGTTTTAAACAATTATAAAAAAGGAG  
TTGGATAA

25

(SEQ ID NO: 62)

MLVSSLVSCSFLLVISSLSSSTRNKSINLSNNFIDLLYQFSIKCYNKTMSFSLKIR  
NPYGEHTVKELLEDYFLIPRKIRHFLRVKKHVLINNEFINWQTVVQENDTITLIF  
DDEDYPTKKIPLGRAELIDCLYEDEHLIIVNKPEGMKTHGNQPNEIALLNHVSA  
30 YSGQTCYVVHRLDMETSGAVLFAKNPFILPLINQRLERKEIWREYWALVEGKF  
SPKHQVLRDKIGRNRHRRKRIDSKNQHAMTIIDVLKYIQNSSLIKCRLETG  
RTHQIRIHLSHHGHPLIGDPLYNPSSNNERLMLHAHRLTLSHPLTCETISVEAPS  
STFEKVLNNYKKGVG\*

35

Sequence description:

- 40 A] Length: 1029 bp - 343 aa (Full length gene sequence)  
B] No obvious Shine-Dalgarno sequence upstream  
of the putative TTG start codon. Possesses a  
potential leader peptide sequence.

ID-107

Clone 2-54

5 (SEQ ID NO: 63)  
GAACTAAATGCAACTCAACCTAATAATAGAACTACCTATATTATACCCGAA  
AGCAGTCATTCCATTGCAGAACAACAGAGATTCCTGATAGAATCAAAGGG  
TTCTTCGGTTGCATTACTTAATAGCGATGAATTTAGAAAGACAGCGGGAGA  
GGATAGAGGTTTTGAAAGGGATAAGTTGAGGTCTTTGGATATCATTCCCTAA  
10 GGGAGATTTATCGACAAGTAATGTCATAGGTAATACGGACATTGCTAGTC  
AGATATCGTTGGGCTTTAAAAAGAATGCGATGCAGGAACACCATCTTACT  
AAAACATTCTCTCAAAAGGATGGAAAGTTATCGTCTGTTATAGAGGGGAT  
GCTTGCTATTGGCAAAGAGAAAAGTAGAGAAAAGAAATAAAATATAGTGGTA  
ATTTATGGCAAAAATTAAGCTAAGGCACACTGCCTTGTTTGCTGTGTG  
15 ATAATTTGAATTTTGAAGATATAAAATCTTATTTTCAATATTATTGTCATCT  
AAACCATCAGCTCAAATTACCTAAAGGTGCTATACTTTCTGCTAAAACAGA  
AGTATATAGGGGAGGAGATTTTGGGAGAAAAAATAAAGATAATGTGTTTG  
GTTACCGTATCCCCTCATTATTGAAAACCCAAAAAGGAACCTTTACTTGCGG  
GAGCTGATGAAAGAATTGAGCAAGCTTGTGATTGGGGAAACATAGGAATG  
20 GTTATTCGCCGTAGTGAGGATGATGGTGTCACTTGGGGAAAAAGAGAAAC  
TATTGTCAATCTCCGTAATAACCCTAGAGTTCCGCTAGTTACTAGTGGTGA  
CTATAGTGGCTCACCTATTAATATGGATATGGCATTAGTTCAAGATACTAG  
CTCCAAGACGAAACGTATTTTTTTCAATATATGATATGTTTCCAGAAGGAAG  
AGGCGTTATTAGTATTGCTAACACACCTGAAAAAGAATATACCCAAATCG  
25 GAGGACAGTCTTATCTTAATTTATATAATAATGGAAAGAAATCGAAGGTTT  
TTACTATCCGTGACAAAGGTATTGTATATAATTTTAAAGGGAAAAAGACTG  
ATTATCATGTTATAACAGAACTACTAAAAGTGACCATTCAAATCTAGGGG  
ATATTTATAAGGGAAAAACAGCTACTTGGAAATATATATTTTACAAAACATA  
AAACGTCACCATTTTCGTTTAGCAAAATCAAGCTATGTGTGGATGTCATATA  
30 GCGATGATGATGGTAGGACATGGTCATCACCTAGAGATATAACAGCAAGT  
CTTCGTCAGAAAGGCATGAAATTTTTTGGGAATAGGACCTGGAAAAGGTAT  
AGTTTTAAATGGGGGCCACACGCTGGTCGTATTATTATTCCTGCCTATTCT  
ACGAATTGGAAATCTCATCTAAGAGGTTCACAATCTTCACGCCTAATTTAT  
TCAGACGACCATGGAAAAACGTGGCATACTGGAAAAGCAGTTAATGATAA  
35 CCGTATACTTTCTAATGGTGAAAAAATTCACCTCCTTAACAATGGATAATAA  
AAAAGAACAAAATACAGAATCCGTACCCGTTCAATTGAAAAATGGGGACA  
TTAAGTTATTTATGAGGAATCTAACTGGTAACCTAGAAGTAGCCACAAGTA  
AAGACGGCGGGGAGACTTGGCAAAACCATGTTAAACGATATAAGGAAATT  
CATGATGCTTAAGTCCAATATCAGCTATTCGCTTTGAGCATGACAAAAAA  
40 GAGTATATTTTATTAGTGAATGCTAATGGGCCAGGGAAGAAGTGCCAAGA  
TGGATATGCACGTCTAGCGCAAGTTAATCGAAATGGTAGTTTAAAGTGGTT  
ATATCACCATCACATTCAAGATGGTTCGTTTGCTTACAACCTCTGTTCAACA  
ACTTAATAATGATCAATTTGGTGTCTTTATGAACATAGAGAAAAACATCA  
AAATAGTTTTACTTTAAATTACAAAGTTTTTAATTGGAGTTTTCTTAGTCAA

AATACAGAGAAGCAAGGCACTTTATGGGAGAAAATGGCAGCAAATTGGCA  
TGTTTTGTTTAAATTTTATTTATGA

(SEQ ID NO: 64)

5 ELNATQPNNRRTTYIIPESHSIAEQQRFLIESKGSSVALLNSDEFKRTAGEDRGF  
ERDKLRSLDIIPKGDLDSTSNVIGNTDIASQISLGFKKNAMQEHLTKTFSQKDG  
KLSSVIEGMLAIGKEKVEKEIKYSGNLWQKLKAKAHCLVCCVDNLNFEDIKS  
YFQYYCHLNHQLKLPKGAILSaktevyrGGDFGRKNKDNVFGYRIPSLKKTQ  
10 KGTLLAGADERIEQACDWGNIGMVIRSEDDGVTWGWKRETIVNLRNNPRVPL  
VTSGDYSGSPINMDMALVQDTSSKTKRIFSIYDMFPEGRGVISIANTPEKEYTQI  
GGQSYLNLNNGKKS KVFTIRDKGIVYNFKGKKTDYHVITETTKSDHSNLGDI  
YKKGQLLGNIYFTKHKTSPFRLAKSSYVWMSYSDDDGRTWSSPRDITASLRQ  
KGMKFLGIGPGKGIVLKWGPHAGRIIPAYSTNWKSHLRGSQSSRLIYSDDHG  
15 KTWHTGKAVNDNRILSNGEKIHSITMDNKKEQNTESVPVQLKNGDIKLFMRN  
LTGNLEVATSKDGGGETWQNHVKRYKEIHDA YVQLSAIRFEHDKKEYILLVNA  
NGPGKKCQDGYARLAQVNRNGSFKWLYHHHIQDGSFA YNSVQQLNNDQFG  
VLYEHREKHQNSFTLNYKVFNWSFLSQNTTEKQGT LW EKMAANWHVLFKFYL  
\*

20 Sequence description:

A) Length: 2052 bp - 684 aa (partial gene sequence)

B) N-terminus has yet to be determined

25

ID-108

Clone 2-61

30

(SEQ ID NO: 65)

ATGCCTAAATTAATCGTATCTTTCCTCTGCATTTTATTATCCCTGACTTGTG  
TAAACTCTGTGCAAGCTGAAGAACATAAAGATATTATGCAAATTACCCGA  
GAAGCCGGATATGATGTAAAGATATTAATAAACCTAAAGCGTCTATCGTT  
ATTGACAATAAAGGTCATATTTTGTGGGAAGATAACGCCGATTTAGAACGT  
35 GATCCCGCTAGCATGTCTAAAATGTTTACTTTATATTTACTATTTGAAGACT  
TAGCTAAAGGAAAAACAAACCTCAACACCACAGTGACTGCAACAGAAACA  
GACCAAGCCATAAGTAAGATTTATGAAATTAGTAATAACAATATTCATGCT  
GGGGTTGCTTATCCTATTCGTGAAGTACTATGACGGCTGTCCCGTCA  
TCTAATGTAGCAACTATTATGATTGCTAACCACTTATCACAAAACAATCCT  
40 GACGCCTTTATTAAACGAATCAATGAAACCGCCAAGAACTCGGTATGAC  
AAAACTCACTTTTATAACCCCAGTGGGGCGGTAGCGAGTGCTTTTAATGG  
ACTTTACTCCCCAAAAGAATACGATAACAATGCTACTAACGTTACGACTGC  
ACGTGATCTATCAATTTTAACCTATCATTTTCCTTAAAAAATAACCCTGATATA  
CTGAACATACAAAATATCCTGAAGTCAAGGCCATGGTCGGAACCTCCTTAT

GAAGAAACATTTACAACCTTATAACTACTCTACCCCCGGCGCTAAATTTGGA  
TTAGAAGGAGTAGATGGCTTAAAACTGGTTCTAGCCCTAGCGCTGCTTTT  
AATGCCTTAGTTACAGCTAAACGCCAGAATACTCGCTTGATAACTGTGGTT  
TTAGGAGTTGGCGATTGGTCAGACCAAGACGGAGAGTACTATCGTCATCC  
5 GTTTGTCAACGCTCTTGTAGAAAAAGGTTTTAAAGACGCTAAAAATATTTT  
TTCTAAAACTCCTGTATTAAGCCGTTAAACCTAAAAAAGAAGTTACTAA  
AACCAAACTAAATCTATTCAAGAACAGCCTCAAACAAAAGAAGAGTGGT  
GGACAAAAACAGATCAATTTATCCAATCACATTTTGTATCTATTTTAATTG  
TTCTGGGCACCATCGCTAGCCTTTGTCTTTTAGCTGGGATAGTATTACTTAT  
10 AAAGCGCTCTAGATAA

(SEQ ID NO: 66)  
MPKLIVSFLCILLSLTCVNSVQAEHKDIMQITREAGYDVKDINKPKASIVIDN  
KGHILWEDNADLERDPASMSKMFTLYLLFEDLAKGKTNLNTTVTATETDQAI  
15 SKIYEISNNNIHAGVAYPELITMTAVPSSNVATIMIANHLSQNNPDFAIKRINE  
TAKKLGMTKTHFYNP SGAVASAFNGLYSPKEYDNNATNVTTARDLSILTYHF  
LKKYPDILNYTKYPEVKAMVGTPYEETFTTYNYSTPGAKFGLEGVDGLKTGS  
SPSAAFNALVTAKRQNTRLITVVLGVGDWSDQDGEYYRHPFVNALVEKGFK  
DAKNISSKTPVLKAVKPKKEVTKTKTKSIQEQPQTKEQWWTKTDQFIQSHFVS  
20 ILIVLGTIASLCLLAGIVLLIKRSR\*

Sequence description:

25 A) Length: 1188 bp - 396 aa (full length gene)  
B) Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

30 ID-109

Clone 45

35 (SEQ ID NO: 67)  
ATGACTGAAAAATATTATAATTGGGCAACGCTTGGAACCGGCGTTATTGCC  
AACGAATTAGCCCAAGCACTGGAAGCACGTGGACAAAAATTATATTCTGT  
AGCTAATAGAACTTACGACAAAGGACTTGAATTTGCTAACAAATATGGTA  
TCCAAAAAGTTTATGATCACATAGATCAAGTATTTGAAGACCCCTGAAGTGG  
40 ATATCATTTATATCTCTACTCCCCACAATACTCACATCTCATTTTTACGAAA  
GGCTTTAGCAAATGGTAAGCACGTTCTTTGCGAAAAATCTATTACTTTAAA  
TAGTACTGAGCTTAAAGAAGCCATAGATTTAGCCGAACTAACCATGTTGT  
CTTAGCTGAAGCCATGACTATTTTTCATATGCCAATTTACCGCCAATTA  
AACATTAGTTGATAGTGGAAAATTAGGACCGTTAAAAATGATTCAAATGA



ATTTTCGGAAGTTATAAAGAATATGATATGACTAACCGTTTTTTTCAGTCGTG  
ACCTAGCAGGCGGTGCTTTGCTGGACATTGGTGTTTATGCACTTTCTTGTAT  
TCGCTGGTTTATGTCAGAAGCACCTCACAACATTACCTCTCAAGTTACATT  
5 TGCACCAACAGGGGTTGATGAACAAGTTGGTATCCTACTAACCAACCCAG  
CAAATGAGATGGCGACTGTCAGCCTTAGTTTACATGCAAAACAACCTAAA  
CGAGCAACTATCGCTTACGATAAAGGCTACATTGAACTTTTTGAATATCCG  
CGAGGACAAAAGGCAGTTATTACTTATACTGAGGATGGGCATCAAGATAT  
TATCGAAGCTGGCAAAACTGAAAATGCTCTCCAATATGAGGTAGCTGATA  
TGAAGAAGCCATTTTCAGGAAAACTAACCACATGTACTTAAACTATACC  
10 AAAGATGTTATGGATATCATGACACAGCTACGTCAAGAATGGGGATTAC  
CTACCCAGAAGAAGAAAAATGA

(SEQ ID NO: 68)

15 MTEKYYNWATLGTGVIANELAQALEARGQKLYSVANRTYDKGLEFANKYGI  
QKVYDHDIDQVFEDPEVDIIYISTPHNTHISFLRKALANGKHVLCESITLNSTEL  
KEAIDLAETNHVVLAEAMTIFHMPYRQLKTLVDSGKLGPLKMIQMNFGSYK  
EYDMTNRFFSRDLAGGALLDIGVYALSCIRWFMSEAPHNITSQVTFAPTGVDE  
QVGILLTNPANEMATVSLSLHAKQPKRATIAYDKGYIELFEYPRGQKAVITYT  
EDGHQDIIIEAGKTENALQYEVAADMEEAISGKTNHMYLNYTKDVMDIMTQLR  
20 QEWGFTYPEEEK\*

Sequence description:

25 A] Length: 984 bp - 328 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

30 ID-110

Clone 2-2

35 (SEQ ID NO: 69)

GTGTATTCTCCTGTAAATCTTCTAAAGGAAAAGTGATATTGTTAAAAAGT  
GATTTTCTAAAGAGCTTCATAGAAAGGAGAGGAAATATTTGTTTT

(SEQ ID NO: 70)

40 MYSPVKSSKGKVILLKSDFLKSFIERRGNICF

Sequence description:



A] Length: 96 bp - 32 aa (partial sequence)  
B] GTG start codon - no obvious Shine-Dalgarno  
sequence  
Possesses a potential signal peptide

5

ID-111

Clone 2-3

10

(SEQ ID NO: 71)

AAATACTGTATCATTGCAACCTCAAATGCAGGTTTTGGAAACGAAGCATTT  
ACAGGTGACAGCGATAAAGACTTGAAAATTATGGAACGAATTTCTCCATA  
TTTCCGTCCAGAATTTCTAAATCGTTTCAATGGTGTTATTGAATTCTCTCAC  
15 CTAAGCAAAGATGACTTAAGCGAAATTGTAGATTTGATGCTTGATGAAGTT  
AACCAAACAATTGGCAAAAAAGGAATTGACCTTGTGGTAGATGAAAATGT  
TAAATCACACTTAATTGAACTGGGTTATGACGAAGCAATGGGAGTACGTC  
CATTGCGCCGTGTCATCGAGCAAGAAATTCGAGATCGCATCACAGACTACT  
ATCTCGATCATACAGACGTTAAACACCTAAAAGCTAATTTGCAAGATGGCC  
20 AAATCGTCATTTCTGAAAGATAA

(SEQ ID NO: 72)

KYCIATSNAGFGNEAFTGDSKDLKIMERISPYFRPEFLNRFNGVIEFSHLSD  
DLSEIVDLMLDEVNQTIGKKGIDLVDENVKSHLIELGYDEAMGVRPLRRVIE  
25 QEIRDRTDYLDHTDVKHLKANLQDGQIVISER\*

Sequence description:

30

A] Length: 429 bp - 143 aa (partial sequence)  
B] N-terminus yet to be elucidated. This gene  
was not in frame with nuc

35

ID-112

Clone 2-5

(SEQ ID NO: 73)

40

ATGTCAATGAATTTTTTCATTTTTACCACAATATTGGTCCTATTTTAATTATG  
GTGTGATGGTAACCATTTATGATTTCAACATGTGTTGTTTTTTTTTGGAACTAT  
TATAGGCGTGTTAATTGCTTTAGTAAAGCGTACTAATTTACATTTTCTCACA  
ATATTAGCTAATTTCTATGTATGGGTATTTTCGTGGGACACCGATGGTAGTT  
CAAATTATGATTGCTTTCGCATGGATGCATTTTAACAATTTACCAACAATT

AGCTTTGGTGTTTTAGATTTAGATTTTACACGACTTTTACCTGGTATCATT  
TCATTTTCCTTAAATAGTGGTGCCTATATTTTCGGAAATTGTACGTGCAGGGA  
TTGAGGCTGTACCATCTGGACAAATAGAAGCAGCTTACTCGTTGGGGATTC  
5 GACCTAAAAATACACTTCGCTATGTTATCTTACCCCAAGCTTTTAAAAATA  
TTTTACCTGCTCTAGGGAATGAATTTATTACAATTATTAAAGATAGTGCTCT  
CCTTCAAACCTATTGGTGTCTATGGAATTATGGAACGGAGCACAATCAGTTGT  
AACGGCTACTTACTCACCAGTTGCACCGTTATTATTTGCAGCATTTTACTAT  
TTAATGTTGACAACGATTCTCTCAGCTTTGTTAAACAAATGGAGAAATAT  
10 CTTGGGAAAGGGGTAAAAATAGATGGTTGA

(SEQ ID NO: 74)  
MSMNFSLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTIL  
ANFYVWVFRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFTRLLPGIIISLNS  
15 GAYISEIVRAGIEAVPSGQIEAAYS LGIRPKNTLRYVILPQAFKNILPALGNEFITI  
IKDSALLQTIGVMELWNGAQSVVTATYSPVAPLLFAAFY YLMLTTILSALLKQ  
MEKYLKGKGVKIDG\*

Sequence description:

20 A] Length: 699 bp - 233 aa (full length gene)  
B] Shine-Dalgarno sequence preceded the 'ATG'  
start codon. Possesses a potential leader peptide  
sequence.

25

ID-113

Clone 2-7

30

(SEQ ID NO: 75)  
ATGAAAGACCTATTACGAAATAGTCTAGAGCAAAGTGGAATTTAAGTTT  
TCAAGATATGATTTTACATATTCTTGTAGCAGCTTTATTGAGTGTAGTTATT  
TATGTTTCCTATGCTTATACGCATAGTGGAAGTGCCTATAGTAAAAAGTTT  
35 AATGTTTCATTAATGACATTGACGGTCTTGACTGCAACAGTAATGACCGTT  
ATTGGTAATAATGTAGCCTTGTCATTGGGTATGGTCGGTGCCTTGTCAGTT  
GTTTCGTTTTAGGACAGCCATAAAAGATTCAAGAGATACAGTTTATATTTTT  
TGGACCATAGTTGTTGGTATCTGTTGTGGTGTCTGGTGACTATGTGGTAGCT  
GCATTAGGAAGTAGCGTTATCTTTATCTTATTATGGGTTATGGGACGTGTT  
40 AAAAACGAGAATCGTATGTTATTGATTGTGAAGTGCGATAGAACTAGA  
AGTTGATTTAGAAGGAATTTTCTTCCAATATTTTGACGGAAAAGCTGTTCA  
GCGTGTTAAAAATTCAACAATACTATTGAAATGATTTTCGAAATCTC  
TAGAAAAGATTACGATAAGCAACTCCATGTAGATAATCAGTTAACTGAAA

AAGTGTACCAATTGGGAAATATTGATTATTTCAACATTGTTAGCCAAAGCG  
ACGAAATCAATGGGTAG

(SEQ ID NO: 76)

5 MKDLLRNSLEQSGNLSFQDMILHILVAALLSVVIYVSYAYTHSGTAYSKKFNV  
SLMTLTVLTATVMTVIGNNVALSLGMVGALSVVRFRTAIKDSRDTVYIFWTIV  
VGICCGVG DYVVAALGSSVIFILLWVMGRVKNNRMLLIVKCDRTLEVDLEGI  
FFQYFDGKAVQRVKNSTTNTIEMIFEISRKDYDKQLHVDNQLTEKVYQLGNID  
10 YFNIVSQSDEING\*

Sequence description:

15 A] Length: 678 bp - 226 aa (full-length gene)  
B] ATG start codon is preceded by a Shine-  
Dalgarno sequence-Possesses a potential leader  
peptide sequence

20 ID-114

Clone 2-8

(SEQ ID NO: 77)

25 AAAAATTCATTTTAGATTCATTTTACGACTATATACTCAGAAGTACCAAAC  
CTAATCCAAGGTTTGAAAAAAGAAAGAAGGAAGTCAGTATGACAAACTAT  
AAAAACAAC TTAAAGATGAGGCTATACGTGTTGAAGAGACAACAAAAGA  
ATCATTTTACGATGTTGATATTGCCTTGTTTTTCAGCTGGTGGATCTATTTCA  
30 GCAAAGTTCGCTCCTTATGCAGTAAAGTCTGGAGCAGTTGTAGTAGATAAC  
ACGTCATATTTTCGTCAGAAATCCTGATGTTCCACTAGTTGTTCCCTGAAGTAA  
ATGCTCATGCCATGATTGGTCATAATGGTATCATAGCTTGTCCCAATTGTTT  
TACTATTCAAATGATGATTGCTTTAGAGCCCATTCGTCAAAAATGGGGGAT  
AGAGCGTGTTATAGTTTCCACCTATCAAGCTGTTTCGGGTTTCAGGTGCACG  
35 TGCTGTTGAAGAACTAAGGAACAGTTGAGACAAGTTTT

(SEQ ID NO: 78)

KFILDSFYDYILRSTKPNPRFEKRKKEVSMTNYKNNFKDEAIRVEETTKESFYD  
VDIALFSAGGSISAKFAPYAVKSGAVVVDNTSYFRQNPVPLVVPEVNAHAMI  
40 GHNGIACPN CSTIQMMIALEPIRQKWGIERVIVSTYQAVSGSGARAVEETKEQ  
LRQV

Sequence description:

A] Length: 499 bp - 165 aa (partial sequence)  
B] N-terminus has yet to be determined

5 ID-115

Clone 2-9

(SEQ ID NO: 79)

10 ATGACAAATGAATTGATAATGCAAGCTTTTGAGTGGTATTTACCTAGTGAT  
GGGAATCACTGGAAGAAATTAGAGGAGTCTATATCAGACCTTAAAAAACT  
TGGAATTAGTAAAATCTGGTTACCACCAGCATTTAAGGGAACTAGCAGTG  
ATGATGTAGGATATGGTGTTTATGATCTCTTTGATTTAGGAGAATTTGACC  
15 AGAATGGAACAATTAGAACAAAATATGGTAGGAAAGAAGAGTATCTAAA  
GCTTATTAAGTCGTTAAAGGCCAAATGGCATTAAACCGTTTGCAGATATCGT  
TCTTAACCATAAAGCCAATGGTGATCATAAAGAAAAATTTCAAGTCATCA  
AAGTCAATCCTGAAAATCGTCAAGAAGCATTAAAGTGAACCCTATGAGATT  
GAAGGATGGACGGGATTTGATTTCCCAGGTAGACAGGGTGAGTACAATGA  
TTTT

20

(SEQ ID NO: 80)

MTNELIMQAFEWYLPDGNHWKKLEESISDLKKLGISKIWLPPAFKGTSSDDV  
GYGVYDLFDLGEFDQNGTIRTKYGRKEEYKLIKSLKANGIKPFADIVLNHKA  
25 NGDHKEKFQVIKVNPNRQEALSEPYEIEGWTGFDFPGRQGEYNDF

25

Sequence description:

30 A] Length: 456 bp - 152 aa (partial sequence)  
B] ATG start codon is preceded by a Shine-  
Dalgarno sequence, no leader peptide sequence.

35 ID-116

Clone 2-10

(SEQ ID NO: 81)

40 ATGGAGGTTCTTATGAAGAAAGTGTTAGTAAGTAGTCTTTTGGTTTTAGGG  
ATTACGATAACGTTACAACCAGTAGTTGAGGCTAAGGGGGCCAAAAGTAGC  
TTATACACAAGAGGGAATGACTGCTCTTTCGGACACAAATAAAGATAAAG  
TCACTACTATTTCTATTGACGAGATTCAAAAAAGCTTAGAAGGTAAGAAGC  
CGATTACTGTTAGTTTTGATATTGATGATACTGCTTTTCAGTAGTCAATA

TTTTCAATATGGTAAAGAATATGTAACCTCGGATCGTTTGATTTTCTTCAT  
AAACAAAAATTCTGGGATCTTGTTGCAAAACGAGGAGATCAAGATTCCAT  
TCCCAAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAG  
ATAAAATTGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAG  
5 GGCGAGGTTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTTGTA  
CCATCTGAT

(SEQ ID NO: 82)

10 MEVLMKKVLVSSLLVLGITITLQPVVEAKGPKVAYTQEGMTALSDTNKDKVT  
TISIDEIQKSLEGKKPITVSFDIDTLLFSSQYFQYGKEYVTPGSFDLHKQKFW  
DLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGSMYKEGEVDKTA  
KALAKDFKFVPSD

15 Sequence description:

A] Length: 516 bp - 172 aa (partial sequence)  
B] ATG start codon is preceded by a Shine-  
20 Dalgarno sequence, Possesses a leader peptide  
sequence.

ID-117

25 Clone 2-17

(SEQ ID NO: 83)

ATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGACAAAGATTAGTCGT  
CGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTATTATTGTCAGGATGT  
30 GTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAACTCCGAATGTTTCAGC  
GCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAATTCTTTTCGTAGTTT  
AGATCAGCTAACTAGCTTTAAAGAGATTCTTTGGGTATTGGTCAAAATGT  
AGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGTTACTATCCCTAAAG  
CCAAGTTTACGGAAATATAAAAGCGTTATATTACTTGCTTTCTTGATGTCTC  
35 TTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTTAATAGATGCTAATCG  
GGTTTTTGAAATCGACGATCTATGGACAAATACCTTAGGCGGTCCTTTTCGC  
CCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCTAACTATTAGAAAATG  
A

40 (SEQ ID NO: 84)

MLKRLFTEDGELTKISRRFVWMLVVIYCLIIVRMCFGPQIMIEGVSTPNVQRF  
RIVALLVPFNSFRSLDQLTSFKEILWVIGQNVVNILLFPLIIGLLSLKPSLRKYK  
SVILLAFMLSLFIECTQVVLDILIDANRVFEIDDLWTNTLGGPFALWSYRNIKG  
WLLTIRK\*

Sequence description:

- 5           A] Length: 516 bp - 172 aa (full-length gene)  
           B] ATG start codon is preceded by an Shine-  
              Dalgarno sequence. Possesses a potential leader  
              peptide sequence. C-terminus need further  
10           confirmation.

ID-118

Clone 3-3

- 15           (SEQ ID NO: 85)  
           ATGAAAAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTTCG  
           TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA  
           ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGG  
20           CAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACT  
           GAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT  
           TAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAAGAACAAGATATT  
           CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTCAGTGTTGGAA  
           ACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTCGGGAT  
25           TCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATT  
           CTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGG  
           AGGTTGCTCAAAAATGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATT  
           CCAAAGAAAACCTATAATTTCAAGTCTCAAAGATATAATATCACTTGATT  
           TCACTCGTTTGGATTAA  
30             
           (SEQ ID NO: 86)  
           MKKLTFIWDLDGTLIDSYPIMEALEETYRHFGLIFDKELIHEYILQESVGQLL  
           VNLSEEEQIPHEKLKAYFTKEQESRDSKIHLMPLYAKEILEWTKEQDIPNFMYTH  
           KGASTHSVLETLOISHYFDEILTVSGFERKPHPQGINYLVKRYSLDKSMTYYI  
35           GDRPLDLEVAQNAGIKSINLRLNSKENYNISLKDIIISLDFTRLD\*

Sequence description:

- 40           A] Length: 627 bp - 209 aa (Possible Full-length gene)  
           B] ATG start codon is preceded by an possible  
              Shine-Dalgarno sequence. No obvious leader  
              peptide sequence.

ID-119

Clone 3-7

5

(SEQ ID NO: 87)

ATGGAAAAAGAAAAAAATTAGGTCTTTTACCACTAACAATGCTTGTCATT  
GGCTCTCTTATCGGTGGCGGAATCTTTGATTTAATGCAAAATATGAGTTCC  
AGAGCCGGTTTGGTACCAATGCTTATTGCTTGGGTAATTACTGCTATCGGG  
10 ATGGGAACTTTTCGTTTTAAGTTTTCAAAATTTATCTGAAAAAAGGCCGGAC  
CTAACAGCTGGAATCTTTAGTTACGCTAAAGAGGGGTTTGGAACTTTATG  
GGATTAACTCTGCATGGGGTTATTGGTTATCAGCTTGGCTTGGAAATGTT  
GCCTACGCTGCACTCTTATTCAGTTCACCTCGGTTATTTCTTTAAATTCTTTG  
GTAATGGAAATAATATCATCTCAATTATTGGAGCAAGTATAGTTATTTGGG  
15 TTGTCCATTTCTTAATTTTAAGAGGTGTTAATACAGCTGCATTTATTAATAC  
CGTAGTTACCTTTGCAAAATTAGTACCTGTTATTATTTTCTTAATTTTCAGCG  
TTATTAGCTTTCAAATTTAACATTTTATAGTCTTGATATCTGGGGAAATGGAT  
TACATCAATCAATTTTCAACCAAGTCAATTCAACTATGAAAACCGCTGTTT  
GGGTATTTATTGGTATTGAGGGCGCCGTTGTCTTCTCAGGTCGTGCTAAAA  
20 AACACTCTGATATTGGTAAAGCAAGTATCCTAGCATTATTCACTATGATTT  
CACTTTATGTATTGATTTCTGTTTTATCACTTGGTATCATGTACGTCACGTCAG  
ACTTGCAAACTTAAAAACACCAGCTATGGCTTACGTTCTAGAAAAAGCTGT  
TGGTCACTGGGGTGCTATCTTAGTTAACCTTGGTGTTATCATTTTCAGTATTT  
GGCGCTATTCTTGCTTGGACTTTATTTGCAGCAGAATTACCATATCAAGCT  
25 GCTAAAGAAGGTGCTTTTCCTAAATTTTTTGCAAAAGAAAAATAAAAAACA  
AGCTCCAATCAACTCACTCTTAGTCACTAATCTTTGTGTACAAGCATTCTTA  
ATCACGTTCTTATTCACACAAAGTGCTTATCGTTTTGGTTTCGCATTAGCAT  
CATCTGCTATCTTAATTCCTTATGCTTTTACAGCACTATATCAATTACAATT  
CACACTCCGTGAGGATAAGTCAACTCCAGGACATCAAAAGAATTTAATTA  
30 TCGGTATCCTCGCTACAATCTATGCTGTTTACCTTATCTACGCTGGTGGTTT  
TGATTACTTACTTTTGACAATGATTGCTTATACTCTAGGTATGATTCTCTAT  
ATTAAAATGAGAAAAGATGACAAGCTTGGCGTAATCATGGTCATAGCTGT  
TTCCAGTGTGAAATTGTTATCC

35

(SEQ ID NO: 88)

MEKEKKLGLLPLTMLVIGSLIGGGIFDLMQNMSSRAGLVPMLIAWVITAIGMG  
TFVLSFQNLSEKRPDLTAGIFS YAKEGFGNFMGFNSAWGYWLSAWLGNVAY  
AALLFSSLGYFFKFFGNGNNIISIIGASIVIWVVHFLILRGVNNTAAFINTVVTF  
LVPVIFLISALLAFKFNIFSLDIWGNGLHQSIQVNSTMKTAVVWVFIGIEGAV  
40 VFSGRAKKHSDIGKASILALFTMISLYVLISVLSLIGMSRPELANLKTPAMAYV  
LEKAVGHWGAILVNLGVIIISVFGAILAWTLFAAELPYQAAKEGAFPKFFAKEN  
KNKAPINSLLVTNLCVQAFLITFLTQSA YRFGFALASSAILIPYAFTALYQLQF  
TLREDKSTPGHQKNLIIGILATIYAVYLIYAGGFDYLLLTMIAYTLGMILYIKMR  
KDDKLGVMVIAVSSVKLLS



Sequence description:

5

A] Length: 1356 bp - 452 aa (partial sequence)  
B] ATG start codon is preceded by an possible  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

10

ID-120

Clone 3-8

15

(SEQ ID NO: 89)

ATGAAATTTGAAAAACGGCAGGTCTATTATGTTGTCATAACATTTGCTATT  
TGCTATGCTATACAGGCTTATTGGGGAGCTGTTTCTAATATTTTAACTACGC  
TTCATAAGGCAATATTTTCCTTTTTTTGATGGGAGCTGGAATTGCCTATATTAT  
20 TAATATTGTAATGTCAGTCTATGAGCGATTATATATAAAGCTTTTTAAAGG  
ATCTAGACTATTAATGGCAATCAAGCGTAGTGTTTCTATGATTTTATCCTAT  
GCAACTTTTATTGGTTTAATTGTCTGGCTATTTTCAATTGTCATTCCAGATT  
TGATTTCTAGTTTGAGTTCCTTTATTGGTTATTGATACCGGAGCACTTGCTAA  
ATTGGTTAATAATCTCAATGAAAATAAACAATTTCTGAGGCTTTAAATTA  
25 TATGGGAACAGATAAAGACTTAGTTTCTACTTTAAGTGTTATAGCCAGCA  
GATTTTGAAGCAAGTTTTATCTGTTTTTAACAAATTTACTAACCTCAGTTTCC  
TCTATTGCGGCAACACTTCTGAATGTTTTTGTTAGTTTTATTTTTCAATTTA  
CGTTTTGGCAAACAAGGAGCAGTTGGGACGTCAATTTAATTTGTTAATTGA  
TACCTATTTAGGTTCAACAGGCAAAACATTCCATTACGTTTCGTCATATCCTT  
30 CATCAACGTTTCCATGGTTTTTTTTGTAAGCCAAACTTTAGAAGCTATGATTT  
TAGGAAGTTTGACGGTTATTGGTATGTTGATCTTCCAATTTCTTATGCTTT  
AACAGTTGGGGTTTTAGTTGCTTTTACAGCTCTAATACCGGTTGTGGGAGC  
CTACATTGGTGTTACAATCGGTTTCATCTTAATTGCTACTGAATCGCTTACT  
GAAGCATTCTTGTTTGTTCTTTTCTTGATCCTTTTACAACAATTTGAGGGAA  
35 ATGTCATTTATCCGAAAGTTGTCTGGTGGATCGATTGGACTGCCTTCTATGT  
GGGTTTTAATGGCTATTACTATCGGAGGTGCTTTATGGGGGATCTTAGGCA  
TGTTACTTGCTGTTCCCTGTTGCAGCTACTATCTATCAGATTGTAAAAGATCA  
TATTATCAAGCGACAAACGCTTAGAAATCGTGCACGAACCTATCGTTAA

40

(SEQ ID NO: 90)

MKFEKRQVYYVVTFAICYAIQAYWGAVSNIL TTLHKAIFPFLMGAGIAYIINI  
VMSVYERLYIKLFKGSRLMAIKRSVSMILSYATFIGLIVWLFSIVIPDLISSLSS  
LLVIDTGALAKLVNNLNENKQISEALNYMGTDKDLVSTLSGYSQQILKQVLSV  
LTNLLTSVSSIAATLLNVFVSFISYVLANKEQLGRQFNLLIDTYLGSTGKTFH

YVRHILHQRFHGFFVSQTL EAMILGSLTVIGMLIFQFPYALT VGV LVAFTALIP  
VVGAYIGVTIGFIL IATESL TEAFLFVLFLILLQQFEGNVIYPKVVGGSIGLPSM  
WVLMAITIGGALWGILGMLLAVPVAATIQIVKDHIKRQTLRNRARTYR\*

5

Sequence description:

- 10                   A] Length: 1134 bp - 378 aa (full-length gene)  
                  B] ATG start codon is preceded by an typical  
                  Shine-Dalgarno sequence. Possesses a potential  
                  leader peptide sequence.

15           ID-121

Identical to ID-68, as described in WO 00/06736

20

ID-122

Clone 3-16

25

(SEQ ID NO: 91)

GTGATTACAATTAAAAAGGAATCTGTTATCAAAC TATTGAAGTATGCTTTT  
GGCATTATAATGGGATTTATTATCTTAGCTATTGTAATAGGTGGGCTCCTA  
TTTGCATACTACGTTAGTCGTTCTCCGAAATTAACCGATCAAGCTTTAAAA  
TCCGTTAACTCTAGTTTGGTTTATGATGGTAATAATAAACTTATTGCCGATT  
30 TAGGCTCAGAAAAGCGTGAAAGTGTTAGTGCGGATAGCATTCCACTAAAT  
TTGGTTAACGCTATCACTTCTATAGAAGATAAACGTTTCTTTAAACATAGA  
GGTGTTCGATATTTATCGTATTTTAGGTGCAGCTTGGCATAACCTTGTTAGTA  
GTAATACGCAAGGTGGTTCAACCCTTGATCAACAGTTGATTAAACTGGCTT  
ACTTTTCTACCAATAAATCTGACCAAACGTTAAAACGTAAATCACAGGAA  
35 GTTTGGCTTGCGCTTCAAATGGAGCGTAAATACACCAAAGAAGAAATTCTT  
ACTTTCTATATTAATAAAAGTTTATATGGGAAATGGGAATTATGGTATGAGA  
ACAACAGCTAAATCATACTTTGGTAAAGACCTAAAGGAATTATCTATTGCA  
CAACTTGCTTTGCTCGCTGGTATTCCTCAAGCACCTACACAATATGACCCTT  
ATAAAAACCCAGAATCTGCTCAAACAAGACGTAATACCGTTCCTCAGCAG  
40 ATGTATCAAGATAAAAACATTTCTAAAAAGGAATACGACCAAGCTGTTGC  
AACTCCAGTAACTGATGGCTTAAAAGAATTAAAGCAAAAATCTACTTATCC  
AAAATATATGGATAACTACTTAAAACAAGTTATTAGTGAAGTTAAACAAA  
AAACTGGTAAAGATATCTTTACTGCTGGGCTAAAAGTGTATACTAATATCA  
ACACTGATGCACAAAAACA ACTATATGACATCTACAACAGTGATACTTAC

ATCGCTTATCCAAACAATGAATTACAAATAGCATCTACCATCATGGATGCG  
ACTAATGGTAAAGTCATTGCACAATTAGGCGGGCGTCATCAGAATGAAAA  
TATTTCAATTTGGGACAAATCAATCTGTCTTAACAGACCGCGATTGGGGTTC  
TACAATGAAACCTATCTCAGCTTATGCACCTGCTATTGATAGTGGTGTCTA  
5 TAATTCAACAGGTCAATCATTAAACGACTCAGTTTACTACTGGCCTGGTAC  
TTCTACTCAACTATATGACTGGGATCGTCAATATATGGGTTGGATGAGTAT  
GCAGACCGCTATTCAACAATCACGTAACGTCCTGCTGTCAGAGCACTTGA  
AGCCGCTGGATTAGACGAAGCAAAATCTTTCCTTGAAAAATTAGGCATAT  
ACTATCCAGAAATG

10

(SEQ ID NO: 92)

MITIKKESVIKLLKYAFGIIMGFIILAIVIGGLLFAYYVSRSPKLTQALKSVNSS  
LVYDGNNKLIADLGSEKRESVSADSIPLNLVNAITSIEDKRFFKHARGVDIYRILG  
AAWHNLVSSNTQGGSTLDQQLIKLAYFSTNKSDQTLKRKSQEVWLALQMER  
15 KYTKEEILTFYINKVYMGNGNYGMRTTAKSYFGKDLKELSIAQLALLAGIPQA  
PTQYDPYKNPESAQTRRNTVLQQMYQDKNISKKEYDQAVATPVTGDLKELK  
QKSTYPKYMDNYLKQVISEVKQKTGKDIFTAGLKVYTNINTDAQKQLYDIYN  
SDTYIAYPNNELQIASTIMDATNGKVIAQLGGRHQENENISFGTNQSVLTDRDW  
GSTMKPISAYAPAIDSGVYNSTGQSLNDSVYYWPGTSTQLYDWDRQYMGWM  
20 SMQTAIQSRNVPAVRALEAAGLDEAKSFLEKLGIIYPEM

Sequence description:

25 A] Length: 1386 bp - 462 aa (partial sequence)  
B] GTG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.

30

ID-123

Clone 3-17

35

(SEQ ID NO: 93)

ATGGCTAATGTATATGATTTAGCAAATGAATTAGAACGTGCTGTTTCGTGCT  
TTACCAGAATACCAAGCAGTTTTAACTGCAAAAGCAGCTATTGAAAATGA  
TGCGGATGCACAAGTGCTTTGGCAAGACTTTTTGGCTACCCAATCAAAAGT  
TCAAGAAATGATGCAATCTGGCCAAATGCCAAGTCAAGAAGAACAAGATG  
40 AAATGTCTAACTTGGGGAAAAAATTGAATCCAATGACCTTTTAAAAGTTT  
ATTTTGACCAACAACAACGGTTGTCTGTCTATATGTCTGATATCGAAAAAA  
TTGTCTTTGCACCCATGCAGGACTTGATGTAA

(SEQ ID NO: 94)

MANVYDLANELERAVRALPEYQAVLTAKAAIENDADAQVLWQDFLATQSK  
VQEMMQSGQMPSQEEQDEM SKLGEKIESNDLLKVYFDQQRLSVYMSDIEKI  
VFAPMQDLM\*

5

Sequence description:

- 10                   A) Length: 336 bp - 112 aa (full length sequence)  
                    B) ATG start codon is preceded by an  
                    typical Shine-Dalgarno sequence. No obvious  
                    potential leader peptide sequence.

15

ID-124

Clone 3-26

20

(SEQ ID NO: 95)

ATGGCAGAAATCACAGCTAAACTTGTA AAAAGAATTGCGTGAAAAATCAGG  
TGCAGGCGTTATGGACGCTAAAAAAGCATTAGTAGAACTGATGGTGACC  
TTGATAAAGCGATTGAATTACTTCGCGAAAAAGGTATGGCTAAAGCAGCT  
AAAAAAGCAGACCGTGTTGCTGCTGAAGGTTTAACAGGTGTTTATGTTGAT  
25                   GGTAACGTTGCAGCAGTTATTGAAGTTAA

25

(SEQ ID NO: 96)

MAEITAKLVKELREKSGAGVMDAKKALVETDGDLDKAIELLREKGMAKAAK  
KADRVA AEGLTGVYVDGNVA AVIEV

30

Sequence description:

- 35                   A) Length: 230 bp - 76 aa (partial sequence)  
                    B) ATG start codon is preceded by an  
                    typical Shine-Dalgarno sequence. No obvious  
                    potential leader peptide sequence.

40

ID-125

Clone 3-33

(SEQ ID NO: 97)

ATGATAAAAAACCTGTTATTAACAGGTTTTTTATCATTTAATGACGGAAAA  
CTGGACACAAATTATTTTCTTGTATAATTAAATATATTATTTCTTATCAGG  
AGGTTATGATGACATTAGAGAAACGATTAA

5

(SEQ ID NO: 98)

MIKNLLLTGFLSFNDGKLDTNFYFSCHKYIISYQEVMMTLEKRF

10      Sequence description:

A) Length: 134 bp - 44 aa (partial sequence)

B) ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possible  
potential leader peptide sequence.

15

ID-126

20      Clone 3-41

(SEQ ID NO: 99)

ATGAAAAATAATAAAAAATAATGGTTTTCTGAAAAATTCCTTTATTTACATA  
TTATTGATTATTGCGGTTATTACAACCTTTCAATACTATTAA

25

(SEQ ID NO: 100)

MKNNKNNGFLKNSFIYILLIIAVITTFQYYL

30      Sequence description:

A) Length: 94 bp - 31 aa (partial sequence)

B) ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

35

ID-127

40      Clone 3-42

(SEQ ID NO: 101)

ATGTTAGATATTATCTTATCCGGAATTCGCAAGGATTACTTTGGTCAATTA  
TGGCAATTGGCGTGTTTATCACTTTTCGTATCTTAGACATAGCCGATCTCTC

TGCAGAAGGGGCTTTCCTATGGGGGCTGCAGTTTGCGCCTTATGTATCGT  
TAA

(SEQ ID NO: 102)

5 MLDIILSGISQGLLWSIMAIGVFITFRILDIADLSAEGAFPMGAAVCALCIV

Sequence description:

10 A] Length: 158 bp - 52 aa (partial sequence)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

15 ID-128

Clone 3-43

20 (SEQ ID NO: 103)

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTTAAATGAG  
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC  
CTACTTTTTATTTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC  
GTTATTTAA

25 (SEQ ID NO: 104)

MEMPKRNELLNKEIKMSIDKLRYPKEPESEHDKRPTFYLVVLILVTVAVILSLF

30 Sequence description:

35 A] Length: 161 bp - 53 aa (full-length gene)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

ID-129

40 Clone 3-44

(SEQ ID NO: 105)

GTGGTAAGTAAATTGAGTTTAACAACGATTTTTGCATTGCTATTTTCATCA  
ATGCTAATTTACGCAACACCTCTTATCTTTACAAGTATTGGGGGAACCTTC

TCTGAACGTGGTGGTATCGTCAACGTTGGTTTAGAAGGAATTATGGTAATT  
GGAGCTTTCTCAGGCGTTGTATTTAA

(SEQ ID NO: 106)

5 MVSKLSLTTIFALLFSSMLIYATPLIFTSIGGTFSEGGIVNVGLEGIMVIGAFSG  
VVF

Sequence description:

10

A] Length: 179 bp - 59 aa (partial sequence)  
B] GTG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

15

ID-130

Clone 3-46/47

20

(SEQ ID NO: 107)

ATGAGAATTATTGCAATAACTGAAAAGGTTATAAAAGAACTGTTTCGTGAT  
AAAAGAACACTTGCTATGATGTTTTTAGCACCTATTTTAATTATGTTTTTGA  
TGAATGTTATGTTTTCTGCGAATAGTAATACAAAAGTTAAGATTGGAAC  
25 TTAACGTTAACACGAAGGTCGTTTCAAATTTAGATAATATTAAGCATATTC  
AAGTGAGATCATTTAAATTTAACTCATCTGCTAAAAAAGCACTCAAATCAA  
ATAAAATTGATGCTCTTATTTTCGGAGGACAATAAATCTTATACTGTCTTCT  
ATGCGAATACAGATTCTTCAAAGACGACTTTAACAAGACAAGCTTTTAAA  
ACCGCTGTTAATAACAATGAACAGTAAGGAAGTATTTTCGCAAGTTAAAATT  
30 TTAGCTAATAAGAATCCGAACTAGCACAATCCTTACAAACTCGCTCCAAA  
TATATCAAAGAAAAATATAATTACGGAAATAAAAAATACAGGCTTTTTTGC  
AAAAATGATACCAATACTAATGGGATTTATGGTCTTCTTCTTGGTTTTT

25

30

(SEQ ID NO: 108)

35 MRIIAITEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSAANSNTKVKIGTINV  
NTKVVSNLNLIKHIQVRSFKFNSSAKKALKSNKIDALISEDNKS YTVFYANTDS  
SKTTLTRQAFKTA VNTMNSKELISQVKILANKNP KLAQSLQTRSKYIKEK YNY  
GNKNTGFFAKMIPILMGFMVFFLVF

40

Sequence description:

A] Length: 558 bp - 186 aa (partial sequence)  
B] ATG start codon is preceded by a

possible Shine-Dalgarno sequence. Potential leader peptide sequence. C-terminus has yet to be determined.

5

ID-131

Clone 3-48

10

(SEQ ID NO: 109)

GTGATTATCGTTATGAGTAAACATCAAGAAATTTTGGAGTACCTAGAAAAT  
TTAGCTGTTGGTAAGAGGGTTAGTGTACGCAGTATTTCAAATCATTAA

15

(SEQ ID NO: 110)

MIIVMSKHQEILEYLENLAVGKRVSVRISNHL

Sequence description:

20

A] Length: 100 bp - 33 aa (partial sequence)  
B] GTG start codon is not preceded by a  
obvious Shine-Dalgarno sequence. No obvious  
leader peptide sequence.

25

ID-132

Clone 2-c53

30

(SEQ ID NO: 111)

ATGTATAGAGAAATTACCGCTGTCGAACACGATCGCTTTGTGAGCGAATCC  
AACCAAACAAACCTACTTCAATCTCTTAATTGGCCCAAAGTAAAAGACAA  
CTGGGGTAGTCAATTACTTGGCTTTTTTGACGGTGAAACCCAAATTGCCAG  
CGCTAGTATTCTCATCAAATCACTTCCTCTTGGCTTCTCCATGCTGTATATT  
35 CCGCGTGGACCAATCATGGATTACTCCAATCTAGATATTGTAACCTAAGGTC  
CTTAAGGACCTTAAAGCTTTTGGCAAAAAACAAAGAGCTCTCTTTATCAAG  
TGTGATCCTCTCATCTATTT

40

(SEQ ID NO: 112)

MYREITAVEHDRFVSESNQTNLLQSLNWPVKVDNWGSQLLGFFDGETQIASA  
SILIKSLPLGFSMLYIPRGPIMDYSNLDIVTKVLKDLKAFGKKQRALFIKCDPLI  
Y



Sequence description:

- 5                   A] Length: 326 bp - 108 aa (partial sequence)  
                  B] ATG start codon is preceded by an obvious  
                  Shine-Dalgarno sequence. No obvious leader  
                  peptide sequence.

10

ID-133

Clone 2-c59

15

(SEQ ID NO: 113)

ATGGACAAGAAAAAATCTTAGTAACGGGTATTGTGCCTAAAGAAGGTCT  
AAGAAAGCTTATGGACCGATTTGATGTTACTTATTCAGAAGATCGCCCAT  
TTCACGTGACTATGTGTTAGAGCATTATCTGAATATGACGGATGGTTACT  
CATGGGACAAAAAGGTGATAAAGAGATGATTGATGCAGGTGAAAACCTAC  
20 AAATTATTTCTTT

20

(SEQ ID NO: 114)

MDKKKILVTGIVPKEGLRKLMDRFDVTYSEDRPFSRDYVLEHLSEYDGWLLM  
GQKGDKEMIDAGENLQIIS

25

Sequence description:

- 30                   A] Length: 215 bp - 71 aa (partial sequence)  
                  B] ATG start codon is preceded by an obvious  
                  Shine-Dalgarno sequence. No obvious leader  
                  peptide sequence.

35

ID-134

Clone 2-c62

40

(SEQ ID NO: 115)

ATTTCGAAAGATGACTACCAAAATATTAGTTTTGGACAGGATCCAGAAGTT  
GTTGATTATGCTGGTCTGTTTGAAAAACGCCGTCAGTTTTAGAAAAAGCA  
GTTAAAAATTTCTTGCAAGAAGAGAGAGCTACGAGAATGCTATCTGATTTC  
TTGCAAGAAGAAAAATGGGTAAGTATTTGCTGAATTTATGGCGATCAA

5 AGAACATTTTGGTAATAAGGCGCTTCAAGAATGGGATGACAAGGCTATTA  
TACGCCGCGAAGAAGAAGCCTTAGCAGGATATCGTCAAAAGCTTAGTGAA  
GTGATAAAATATCATGAAGTAACGCAATATTTCTTTTACAAACAATGGTTT  
GAGTTAAAAGAATATGCTAATGATAAAGGGATTCAAATTATCGGTGATAT  
GCCAATCTACGTTTCTGCCGATAGTGTAGAAGTTTGGACAATGCCTGAACT  
GTTT

10 (SEQ ID NO: 116)  
ISKDDYQNISFGQDPEVVDYAGLFEKRRPVLEKAVKNFLQEERATRMLSDFLQ  
EEKWVTDFAEFMAIKEHFGNKALQEWDDKAIIRREEEALAGYRQKLSEVIKY  
HEVTQYFFYKQWFELKEYANDKGIQIIGDMPIYVSADSVEVWTMPELF

15 A] Length: 459 bp - 153 aa (partial sequence)  
B] More sequencing is required to determine the  
N- and C-termini  
enzyme). - *Streptococcus pneumoniae* (63%)

20 ID-135

Identical to ID-108 described in WO 00/06736

25 Clone 2-c63

ID-136

30 Clone 2-c66

(SEQ ID NO: 117)  
ATGGCAAAACAGAAAAATAACTGGCGCCGTGTTGGAGTTGGTGTCTTAC  
ACTTGCTTCAGTTGCGACTCTTGCTGCATGTGGAAGTAAATCAGCTTCCCA  
GGATTCTAATGGAGCGATTAAATTGGGCTATTCCAACAGAAATCAATACACT  
35 AGATTTATCTAAAGTTACAGACACTTACTCAAATCTAGCTATTGGTAACTC  
TAGTAGTAATTTCTTTCGCTTAGATAAAGATGGAAAGACAAGACCAGACTT  
GGCTACTAAAGTTGATGTTTCAAAGATGGCTTAACTTATACAGCTACATT  
ACGTAAAGGCTTGAAGTGGTCAGATGGCAGTAACTTACTGCAAAGGATT  
TTGTTTATTCATGGCAACGTTTAGTTGATCCTAAAACAGCTTCACAATATG  
40 CTTACCTTGCTGTTGAAGGGCATGTGCTTAATGCCGATAAAATCAACGAAG  
GACAAGAGAAAGACTTGAATAAGCTAGGTGTTAAGGCAGAAGGCGATGA  
CAAAGTTGTTATTACTTTATCTAGTCCGTCTCCGCAATTCATCTACTACCTT  
GCATTCACTAACTTCATGCCACAAAAACAAGAAGTTGTTGAAAAATATGG  
AAAAGATTACGCAACTACTTCAAAAAATACAGTTTACTCAGGACCATATA

CTGTTGAAGGTTGGAATGGTTCGAATGGTACTTTCACGCTGAAGAAAAAC  
AAAAATTATTGGGACGCTAAAAATGTAAAAACAAAAGAAGTTCGCATCCA  
GACTGTTAAAAAACCAGATACCGCCGTTCAAATGTATAAACGTGGTGAGT  
5 TAGATGCAGCTAATATCTCAAATACTTCTGCTATTTATCAAGCTAATAAAA  
ATAATAAAGATGTCACAGATGTTCTAGAAGCGACCACTGCCTATATGGAA  
TATAATACTACTGGTTCTGTGAAAGGGCTTGATAATGTTAAGATTCGTCGC  
GCCTTAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGAT  
ACAGGCTCAAAACCGGCAATTGCTTTTGCACCTACTGGTTTAGCCAAAACA  
CCAGATGGAAGTATTTGGCAAAATATGTTGCCCCAGGTTATGAATATAAT  
10 AAAACTGAAGCAGCAAACTCTTTAGACTA

(SEQ ID NO: 118)  
MAKQKNNWRRVGVGVLTLASVATLAACGSKSASQDSNGAINWAIPTEINTLD  
LSKVTDITYSNLAIGNSSSNFLRLDKDGKTRPDLATKVDVSKDGLTYTATLRKG  
15 LKWSDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQEK  
DLNKLGVKAEGDDKVVITLSSPSPQFIYYLAFTNFMPQKQEVVEKYGKDYAT  
TSKNTVYSGPYTVEGWNGSNGTFTLKKKNKYWDAKNVKTKEVRIQTVKKPD  
TAVQMYKRGELDAANISNTSAIYQANKNNKDVTDVLEATTAYMEYNTTGSV  
KGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAK  
20 YVAPGYEYNKTEAAKLFRL

Sequence description:

25 A] Length: 1143 bp - 381 aa (partial sequence)  
B] Shine-Dalgarno sequence precedes ATG codon.  
Possesses a potential leader peptide sequence.

30 ID-137

Clone 2-c67

35 (SEQ ID NO: 119)  
TTGAGAGTTTATGAAAATAAAGAAGAGTTGAAAAAAGAAATAAGTAAAAC  
ATTTGAGAAATACATTATGGAATTTAATAA  
TATTCCAGAGAATCTAAAAGATAAAAGAATTGATGAAGTTGATAGAACTC  
CAGCAGAAAACCTTTCTTATCAGGTTGGCT  
40 GGACCAACTTGGTTCTTAAATGGGAAGAAGATGAAAGAAAGGGACTTCAA  
GTAAAAACACCATCGGATAAATTT

(SEQ ID NO: 120)

MRVYENKEELKKEISKTFEKYIMEFNNIPENLKDKRIDEVDRTPAENLSYQVG  
WTNLVLKWEEDERKGLQVKTPSDKF

5

Sequence description

- 10                   A] Length: 234 bp - 78 aa (partial sequence)  
                    B] TTG start codon is preceded by a  
                    potential Shine-Dalgarno sequence. No obvious  
                    leader peptide sequence.

15           ID-138

Clone 2-c70

(SEQ ID NO: 121)

20   ATGTCAAAGTTTGATAGTCAGAAAATAATTACTCCGATTATGAAGTTTGTC.  
    AATATGCGAGGGATTATTGCACTCAAAGATGGCATGCTAGCAATTTTACCA  
    CTAACAGTTGTTGGGAGTCTCTTTTAAATATTAGGGCAGCTTCCATT

(SEQ ID NO: 122)

25   MSKFDSQKIITPIMK FVNMRGIIALKDGMLAILPLTVVGSFLILGQLPF

Sequence description

- 30                   A] Length: 150 bp - 50 aa (partial sequence)  
                    B] ATG start codon is preceded by a potential  
                    Shine-Dalgarno sequence. Possesses a potential  
                    leader peptide sequence.

35

ID-139

Clone 2-c71

40

(SEQ ID NO: 123)

GAGACCACTTCATCAGTTAAACCAGCAGGAATTGACCGTATCAATCATACC  
TCAACACCCCCGAAGAAAAC TACCCCAACATTGCAACGACGCATAGCTT  
CAAAGATCGTTGTGATACTTTAGAAAGAATT CACAATGAAGACATTGATGT  
TTGTTCTGGATTCATTTGTGGTATGGGAGAGAGCGATGAGGGGCTCATCAC

ATTAGCTTTCAGACTAAAAGAACTGAACCCCTATTCTATCCCTGTCAATTTT  
TTACTTGCTGTTGAAGGAACACCTCTTGGAATAATAACTATTTGACTCCC  
ATTAAATGCTTAAAAATTATGGCCATGTTGCGTTTTGTTTTTCCTTTCAAGG  
AATTAAGATTAAGTGCTGGACGGGAGGTCCATTTTGAGAATTTTGAATCAT  
5 TAGTCACCTTACTTGTTGACTCAACTTTTTTGGGAAATTACCTAACAGAGG  
GGGGTCGCAATCAACATACCGATATTGAATTCTTGGAATAATTACAATA  
AATCATACTAAAAAGGAATTAATTT

(SEQ ID NO: 124)  
10 ETTSSVKPAGIDRINHTSTPPKKTTPNIATTHSFKDRCDTLERIHNEIDVCSGFI  
CGMGESDEGLITLAFRLKELNPYSIPVNFLLA VEGTPLGKYNLYLTPIKCLKIMA  
MLRFVFPFKELRLSAGREVFHNFESLVTLLVDSTFLGNYLTEGGRNQHTDIEF  
LEKLQLNHTKKELI

15  
Sequence description:

20 A] Length: 535 bp - 178 aa (partial sequence)  
B] N- and C-termini require verification

ID-140

25 Clone 2-c73

(SEQ ID NO: 125)  
ATGCCGGTTTGGACTGCACAGTCTATTCCAAAGGCATTTTTAGAAAAGCAT  
AATACTAAGGAAGGCACCTGGGCAAACTAACCATTCTAAGTGGTTCTTTA  
30 GTATTTTACCAGTTATCTCCTGATGGAGAGGAAATCTCGCGGCATATTTT  
GATGCTAGTAGTGATATTCCTTTTGTGATCCACAAGTCTGGCATAAAGTT  
TCGCCGAATAGTCCAGACTTAAGTTGCTATCTAACTTTTTACTGCCAAAAA  
GAAGATTACTTCCATAAAAAATATGGTCTCACGCGCACACATTCTGAGGTT  
ATCGCCAGTGCACCTCTCTTATCTGAGAAGAGTAATATATTAGACCTTGGG  
35 TGTGGTCAAGGGCGAACTCACTTTATTTATCGCTGCTGGGACATCAAGTG  
ACTTCTGTGCGATTCAAACGGACAGAGCCTTG TAGCTTTAGAAAATATGGCA  
TTAGAAGAAGAGCTTCCTTACAATATAAAAAGGTATGATATTAATACTACT  
GCTATTGAAGGGCACTATGATTTTATTTTATCAACTGTGGTATTTATGTTTT  
T

40  
(SEQ ID NO: 126)  
MPVWTAQSIPKAFLEKHNTKEGTWAKLTILSGSLVFYQLSPDGEEISRHIFDAS  
SDIPFVDPQVWHKVSPNSPDLSCYLFYCQKEDYFHKKYGLTRTHSEVIASAP

LLSEKSNILDLGCGQGRNSLYLSLLGHQVTSVDSNGQSLVALENMALEEELPY  
NIKRYDINTTAIEGHYDFILSTVVFMF

5      Sequence description:

A] Length: 563 bp - 187 aa (partial sequence)  
B] N- and C-termini require verification

10

ID-141

Clone 2c76

15

(SEQ ID NO: 127)

ATGACAAAGCAAATAATTGCCATTTGGGCTGAAGATGAAGACCATTTGAT  
TGGAGTTAATGGCGGTTTACCATGGAGGCTTCCTAAAGAGTTACATCACTT  
CAAAGAAACGACCATGGGGCAGGCTTTGCTTATGGGACGAAAGACCTTTG  
20 ATGGAATGAACCGTCGTGTTTTACCTGGTAGAGAGACAATCATCTTAACAA  
AAGATGAACAATTCCAAGCAGATGGAGTGACAGTCCTAAATAGTGTTGAA  
CAAGTTATAAAATGGTTTCAGGAACATAATAAGACCTTATTTATTGTAGGT  
GGTGCAAGTATTTATAAAGCATTCTGCCTTATTGTGAAGCAATCATAAAA  
ACTAAAGTTCATGGAAAATTCAAAGGTGATACCTATTTTCCTGATGTTAAT  
25 CTATCTGAGTTT

(SEQ ID NO: 128)

MTKQIIAIWAEDEDHLIGVNGGLPWRLPKELHHFKETTMGQALLMGRKTFDG  
MNRRVLPGRETIILTKDEQFQADGVTVLNSVEQVIKWFQEHNKTLFIVGGASI  
30 YKAFLPYCEAIKTKVHGKFKGDTYFPDVNLSEF

35

Sequence description:

A] Length: 417 bp - 139 aa (partial sequence)  
B] ATG start codon is preceded by a Shine-  
Dalgarno sequence. No leader peptide sequence

40

ID-142

Clone 2-c78

(SEQ ID NO: 129)

TTGTGGCCAAACTGTGCCCCGCTTATTAATAGCACTTTGTTACCAATTGAA  
GATATCTTAACATCAGGTGCTCATAGCAACCCTATTTTAATGGGGGTTATA  
CTTGGCGGGACAATTGTAGTAGTGGCGACAGCACCACCTTTCTTCTATGGCA  
5 TTGACAGCTATGCTAGGATTAACCGGAATGCCTATGGCTATAGGAGCCTTG  
TCTGTCTTTGGTTCGTCATTTATGAATGGTGTACTTTTCCATAAATTAAAC  
TTGGAAGTCGTAAAGATAATATAGCTTTTGCTGTTGAGCCTCTAACTCAAG  
CTGACGTGACTTCAGCTAACCCTATTCCAATCTATGTCACTAATTTTGTTGG  
TGGTGCAGCTTGTGGTATTTTAATTGCCTTGATGAAATTAGTTAATGATACT  
10 CCTGGAACAGCGACACCAATTGCAGGATTTGCTGTCATGTTTGCCTATAAC  
CCAATGATAAAAGTACTAATAACCGCTCTAGGTTGTATTATCCTATCTTTA  
CTAGCAGGCTATTTTGGAGGCATTGTTTTT

(SEQ ID NO: 130)

15 MWPNCAPLINSTLFTIEDILTSGAHSNPILMGVILGGTIVVVATAPLSSMALTA  
MLGLTGMPMAIGALS VFGSSFMNGVLFHKLKLGSRKDNI AFAVEPLTQADVT  
SANPIPIYVTN FVGGAACGILIALMKLVNDTPGTATPIAGFAVMFAYNPMIKVL  
ITALGCIILSLLAGYFGGIVF

20

Sequence description:

25 A] Length: 540 bp - 180 aa (partial sequence)  
B] N- and C-termini have yet to be elucidated

ID-143

30 Clone 2-c80

(SEQ ID NO: 131)

ATGTTTTTAAGTATAATGGCAGGTGTCATAGCATTTGTCCTGACAGTTATT  
GCCATTCCACGCTTCATTAAGTTTTACCAATTGAAGAAAATTGGCGGGCAA  
35 CAAATGCATGAAGATGTCAAACAACATCTAGCCAAAGCAGGTACGCCGAC  
AATGGGAGGAACGGTATTTT

(SEQ ID NO: 132)

40 MFLSIMAGVIAFVLTVIAIPRFIKFYQLKKIGGQMHEDVKQHLAKAGTPTMG-  
GTVF

Sequence description:

5                   A] Length: 172 bp - 57 aa (partial sequence)  
                  B] Shine Dalgarno sequence precedes 'ATG' start  
                  codon. Possesses a potential leader peptide  
                  sequence.

ID-144

10           Clone 3-83

(SEQ ID NO: 133)  
ATGAAACCATATTTATCTTTTATTGGTAGAACGTTATTATACTTCGGTATTT  
15           TATTGTTACTAATTTACTTTTTTGCATACCTTGGTCGCGGACAAGGCAGTTT  
                  TATTTATAA

(SEQ ID NO: 134)  
MKPYLSFIGRTLTYFGILLLLIYFFAYLGRGQGSFIY

20           Sequence description:

25                   A] Length: 113 bp - 37 aa (partial sequence)  
                  B] Putative ATG start codon is preceded by a  
                  typical Shine-Dalgarno sequence. Possesses a  
                  potential leader peptide sequence.  
                  This orf is not in frame with nuc

30           ID-145

Clone 3-86

35           (SEQ ID NO: 135)  
ATGTCATATTTTAGAAATTACTGGTATCGTTTTGGAGCAATTTTATTTATTA  
TTTTAGCAGTAATATTGCTTGTTTTAGACCTGACTGGTCAATGCTTCACTA  
TCTATTGTATTTTACTTTATGGCACTTCTAGCGCATCAATTTGAAGAATAT  
CAGTTTCCCGGTGGGGCATCACCTATCATTAACCTATGTTGTTTATGATGAA  
40           GAAGAGCTGATGGATTGTTTTCCAGGCAATACTCAGTCTATTATGTTGGTT  
AATACTATTGCTTGGTTGCTTTACATTGCTAGTATTGCTTTTCCTCAAGCTT  
ATTGGCTTGGATTAGGAGTCATGTTCTTTAGTCTAACGCAGCTCTTGGGTC  
ATGGTTTTTCAGATGAATATTAACCTTAAACCTTGGTATAATCCTGGTCTAG  
CAACGACAGTATTTCTCCTAGTACCAATAGCTTGCGCATACATCTATCAAG



CTAGTGCAGAAGGAATGCTCACTTGGGGAGATTGGCTAGGTGGTTTTATCA  
TGTTGATTGTCTGTGTACTAACTAGCATTATTGCACCTGTACAGCTATTGAA  
GGATAAGGAGACCAATTATATTATTAGTCCTTGGCAAATGGACCGTTTTCA  
TAAGGTCGTTAATTTTGTAAGGATAAAAAAATAA

5

(SEQ ID NO: 136)

MSYFRNYWYRFGAILFIILAVILLVFRPDWSMLHYLLYFYFMALLAHQFEEYQ  
FPGGASPIINYVVYDEEELMDCFPGNTQSIMLVNTIAWLLYIASIAFPQAYWLG  
LGVMFFSLTQLLGHGFQMNIKLKTWYNPGLATTVFLVPIACAYIYQASAEG  
MLTWGDWLGGFIMLIVCVLTSIIPVQLLKDKETNYIISPWQMDRFHKVVNFV  
RIKK\*

10

Sequence description:

15

A] Length: 651 bp - 219 aa (full length gene)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.

20

ID-146

25

Clone 3-c88

(SEQ ID NO: 137)

ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTTCATCAAAATTT  
CGCGGTTATAGCGAAGAAGAAGTT

30

(SEQ ID NO: 138)

MPLTALEIKDKTFSSKFRGYSEEEV

35

Sequence description:

A] Length: 75 bp - 25 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No leader  
peptide

40

ID-147

Clone 3-90

(SEQ ID NO: 139)

5 ATGTCACCTTTTTCAAGAAAAAATTGCTTACAATTGCGCTAAAAAGGAAGCG  
CTTTATAAAGAGAGTTTAGGACGCTACGCCTTGAGATCAATGCTAGCAGG  
GGCTTATTTGACAATGAGTACTGCTGCCGGTATCGTCGCAGCTGATACTAT  
TGGTAAAATTTCTCCTGCTCTATCAGGTTTTGTATTTGCTTTTCATCTTTAGTT  
10 TTGGACTTATTTATGTTTTAATATTTAATGGTGAATTGGCGACATCTAATAT  
GCTTTATCTCACTGCAGGAGCCTATAATAAAAAATATCTCTTGAAAAAAGC  
CATAACAATTTTAATTTATTGTACTTTTTTCAACCTCGTTGGTGCTTGTATA  
TTAGCTTGGTTGTTTAA

(SEQ ID NO: 140)

15 MSLFQEKIAYNCAKKEALYKESLGRYALRSMLAGAYLTMSTAAGIVAADTIG  
KISPALSGFVFAFIFSFLIYVLIFNGELATSNMLYLTAGAYNKNISWKKAITILI  
YCTFFNLVGACILAWLF

20 Sequence description

25 A] Length: 406 bp - 125 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possible  
leader peptide

ID-148

30

Clone 3-92

(SEQ ID NO: 141)

35 AAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAACCAGCTTC  
AACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGGCTCCAACCTC  
ATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAA  
TTCAGTACATAACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGC  
AGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACA  
GTAETCTACACAAAATATGGCAGCAAATAACATTTTCAATATGTTATCTGGCA  
40 ACAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTTG  
GAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACCTATGACCACGT  
TCACGTATCATTTAA

(SEQ ID NO: 142)

KLQATEVKSPVVAQPASTTNAVAAHPENAGLQPHVAAAYKEKVASTYGVNEF  
STYRAGDPGDHKGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQ  
KFYSNTNSIYGPANTWNAMPDRGGVTANHYDHSVHVSF

5

Sequence description

10

A] Length: 419 bp - 139 aa (partial sequence)  
B] N- and C-termini have yet to be determined

ID-149

15

Clone 3-94

(SEQ ID NO: 143)

20 ATGATTCCAGTAGTTATTGAACAAACAAGTCGTGGTGAACGTTCTTATGAT  
ATTTACTCACGTCTTTTAAAAGATCGTATTATTATGTTGACAGGCCAAGTT  
GAGGATAATATGGCCAATAGTATCATTGCACAGTTATTGTTTCTCGATGCA  
CAAGATAATACAAAGGATATTTACCTTTATGTCAATACACCAGGTGGTTCA  
GTATCGGCTGGACTTGCTATTGTGGACACCATGAACTTCATTAAATCGGAC  
GTACAGACGATTGTTATGGGGATGGCTGCTTCGATGGGAACCATTATTGCT  
25 TCAAGTGGTGCTAAAGGAAAACGTTTTATGTTACCGAATGCAGAATATATG  
ATCCACCAACCAATGGGCGGAACAGGCGGAGGTACACAGCAATCTGATAT  
GGCTATCGCTGCTGAGCATCTTTTAAAAACGCGTCATACTTTAGAAAAAAT  
CTTAGCTGATAATTCTGGTCAATCTATTGAAAAAGTCCATGATGATGCAGA  
GCGTGATCGTTGGATGAGTGCTCAAGAACACTTGATTATGGCTTTATTGAT  
30 GCTATTATGGAAAATAATAATTTACAATAATAGATTTAAAAGAGTTGAGTT  
TACCAACTCTTTTTTTATTTGTTGGAATTATGTTATAATCTTAGTAATTACA  
GATATGACGCAGAAAGGAAAAAATTATTGA

35

(SEQ ID NO: 144)

MIPVVIEQTSRGERSYDIYSRLLKDRIIMLTGQVEDNMANSIIAQLLFLDAQDN  
TKDIYLYVNTPGGSVSAGLAIVDTMNFIKSDVQTIVMGMAASMGTHIASSGAK  
GKRFMLPNAEYMIHQPMGGTGGGTQQSDMAIAAEHLLKTRHTLEKILADNSG  
QSIEKVHDDAERDRWMSAQEHLIMALLMLLWKIIYNRFRKRVFTNSFFICW  
NYVIILVITDMTQKGKNY\*

40

Sequence description

A] Length: 693 bp - 231 aa (full length gene)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No leader  
peptide. Significantly, it would appear to have a  
very hydrophobic C-terminus.

ID-150

Clone 2-c86

(SEQ ID NO: 145)

ATGAAACCAAAAaTTATTGGTGTACTTGGTCTAGGAATATTTGGACAAACA  
CTCGCACAAGAATAAGTAACCTTTGAACAAGATGTTATTGCTATTGACAGC  
AATCCTGAAAATGTACAAGCTGTCGCCGAAGT  
TGTTACAAAAGCAGCTATCGGAGACATTACTGATTTAGCTTTCCTAAAACA  
CATCGGGATCAGTGACTGTGATACTGTTATTATTGCTACAGGAAACAGTTT  
AGAGAGCTCAGTATTGGCCGTAATGCACTGTAAAAAGTTAGGCGTCCCAC  
AAGTTATTGCTAAAGCTCGAAACCTTGTATACGAAGAAGTACTTTATGAAA  
TTGGTGCTGATTTGGTTATCTCTCCGGAGCGAGAATCTGGGCAAAATGTTG  
CTGCAAACCTCATGAGAAATAAAATTACAGATGTCTTCCAGATTGAATCTG  
ATATTTCTGTCATTGAATTT

(SEQ ID NO: 146)

MKPKIIGVLGLGIFGQTLAQELSNFEQDVIAIDSNPENVQAVAEVVTKAAIGDI  
TDLAFLKHIGISDCDTVIIATGNSLE  
SSVLAVMHCKKLGVPQVIKARNLVYEEVLVEIGADLVISPERESGQNVAAN  
LMRNKITDVFQIESDISVIEF

Sequence description:

A] Length: 459 bp - 153 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.  
This orf is not in frame with nuc

ID-151

Clone 2-c88

(SEQ ID NO: 147)

GTGCGTTATAGTAAAGAGATTATTCAGTTAGCTATACCAGCTATGATTGAA  
AATATCTTACAAATGCTCATGGGAGTAGTTGATAATTATCTAGTGGCTCAG  
TTAGGTGTTGTAGCAGTATCAGGTGTTTCAGTTGCTAATAATATAATTACT  
5 ATTTATCAAGCTATTTTTATAGCTTTAGGGGCGAGTATAGCAAGTCTATTG  
GCCAAGTCGTTAGCAGGTAGTGAGAAGGATGATGCAATTCAGTATGTTCT  
CAAGCCATTTTTCTAACATCACTGATAGGGGCAGTATTAGGAATTATCTCG  
ATTGTTTTTGGACAAACTTTCTTT

(SEQ ID NO: 148)

MRYSKELIQLAIPAMIENILQMLMGVVDNYLVAQLGVVAVSGVSVANNIITIY  
QAIFIALGASIASLLAKSLAGSEKDDAISVCSQAIFLTSLIGAVLGIISIVFGQTF

Sequence description

A] Length: 330 bp - 110 aa (partial sequence)

B] Putative GTG start codon is preceded by a  
typical Shine-Dalgarno sequence. May have a  
leader peptide

ID-152

Clone 2-c92

(SEQ ID NO: 149)

TTGATTAACAAGTATTCGTGCTTTTTGAAGAGGATTCTCCATAATAATACT  
30 CCTTTAATAGTTATCGTGAGAAGTATTTTAAAGAAAAACCGCCAAGGTAG  
AGCGACATTTCTGCCTTTAACTACAATAAAACCAAGAGAATTAGCACAAAC  
ATTATCTCTCAAAATTACAAAGTTCTCAAGGGTTTTTAGGAATAGCTAGTG  
AATTGGTAACCTATGATCAACGCTTGTCAAACATTTTT

(SEQ ID NO: 150)

MINKYSCFLKRILHNNTPLIVIVRSILKKNRQGRATFLPLTTIKPRELAQHLYSK  
LQSSQGFLGIASELVTYDQRLSNIF

Sequence description

A] Length: 240 bp - 80 aa (partial sequence)

B] No obvious Shine Dalgarno sequence precedes the Putative TTG start  
codon

ID-153

5 Clone 2-c94

(SEQ ID NO: 151)

TTGTTGACTCACAAAAATATATTATTAACCATTATATTTGGATTATTTATGA  
TTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATA  
10 ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAAT  
ACTTTTGTTCCCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTG  
ATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTTCAGTGAAAT  
GGCAGCCTATTAACCTGGGATATGAAAGAACTGAACTTAATAATGGTAAT  
15 ATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAA  
AGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAA  
AACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAG  
GAGCCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAACGCTAAACCTGATA  
TTTTAAAAAAGTTTGTAAGGAAAAGAAGCAGTTCAATACGATACTTTC  
20 ACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATT  
GATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAA

(SEQ ID NO: 152)

MLTHKNILLTIIFGLFMILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFV  
PMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKETELNNGNIDLI  
25 WNGYSKTAERAKKVAFNPNMNNHQVIVTKTSSHINSIKDMKGKKLGAQSG  
SSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANY  
YLKQEG

30 Sequence description

35 A] Length: 649 bp - 216 aa (partial sequence)  
B] TTG start codon is preceded by a possible  
typical Shine-Dalgarno sequence. Has a  
leader peptide

40 ID-154

Clone 2-c100

(SEQ ID NO: 153)

ATGAAAATTTGGAAAAAATAACCTTAATGTTTTCTGCAATTATTTTAACA  
ACAGTAATTGCATTGGGAGTCTATGTTGCCTCAGCTTATAATTTTTCGACTA  
ATGAATTGTCTAAGACTTTT

5

(SEQ ID NO: 154)

MKIWKKITLMFSAIILTTVIALGVYVASAYNFSTNELSKTF

10 Sequence description

A] Length: 123 bp - 41 aa (partial sequence)

B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide

15

ID-155

20

Clone 2-c1

(SEQ ID NO: 155)

ATGAAAAAACAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA  
GGAATACCAGGCAGAACAGAATTTTAAGTCATACTTTAAATATATATCAG  
ATAAAAATAACTATTTAGATAATATAAAAGTTTATTACTTTTCTATAAGTA  
TTTCTAAAGATGTACAAGATAAAGTCAGTGAAACAACAACCTTGTTTCATATA  
GACTAGAAAAGCAAAAGAATCAAGAGTTCATTGGTAATTTTGAACATGAA  
GTTAGTGAATCTAGTCAATATTCAACCGAAGTTAAAAATCAAATACAGTAT  
CCAATCCAGTATAAAGATAATTCAATTCGTTTTACTGAAAAAACACCGTCA  
GAACGTTATGATGAGTTTGTGTTTTAGTTCATTTGATTCTTCATTATTA  
AATATAAAATATATGATTACTTACTAAAACATCCCGAACTGAATTA  
GGTGTTTCCTATAAGATTCCTATAAATTCTGAAATTGTAGCCCCTTTTATA  
ATCAATTAAATATAAAAAATCCTAAAAATCATCTATTTCGGTTACAAAA  
CGGAAAGTAAAGAATATTATTATACAATCAGTATTGATACTGATTCTGAGA  
TATATTCTATATTCGAAGGTATTCAT

25

30

35

(SEQ ID NO: 156)

MKKQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYFKYISDKN  
NYLDNIKVYYFSISISKDVQDKVSETTTCYSRLEKQKNQEFIGNFEHEVSESSQ  
YSTEVKNQIQYPIQYKDNSIRFTEKTPSERYDEFVFSSFDSSLLKKYKIYDYLLK  
HPETELKGVSYKIPINSEIVAPFINQLNIKNPKKSSISVTKTESKEYYYTISIDTDS  
EIYSIFEGIH

40

Sequence description

5

A] Length: 687 bp - 229 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide. C-terminus has yet to be  
verified

10

ID-156

15

Clone 2-c5

(SEQ ID NO: 157)

ATGACATTTGACACCATTGATCAATTAGCGGTTAATACAGTCCGCACGCTT  
TCTATTGATGCTATCCAAGCAGCAAATTCTGGGCACCCAGGTCTTCCTATG  
GGAGCTGCGCCTATGGCTTATGTGCTTTGGAATAAATTCTTAAATGTAAAC  
CCAAAAACAAGTCGCAATTGGACAAACCGTGACCGTTTTGTACTTTCAGCT  
GGGCATGGTTCAGCTCTTCTTTATAGCCTACTTCATTAGCTGGCTATGATT  
TATCAATTGATGATTT

20

25

(SEQ ID NO: 158)

MTFDTIDQLAVNTVRTLSIDAIQAANS GH PGLPMGAAPMAYVLWNKFLNVNP  
KTSRNW TNRDRFVLSAGHGSALLYSLHLAGYDLSIDD

30

Sequence description

35

A] Length: 272 bp - 90 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. No obvious  
leader peptide

ID-157

40

Clone 2-c8



(SEQ ID NO: 159)

ATGAGAACACTATTTAGAATGATATTTGCTATTCCAAAGTTTATCTTTAGA  
TTGATTTGGAATATCATTTGGGGAATATTCAAGACAGTTCTTGTTATTGCG  
ATTATTTTATTTGGCTTGTATTACTATGCGAATCACAGTCAATCAGAATTTG  
CTAATCAACTTAGTGACATTATTCAGACAGGAAAAACATTTTT

(SEQ ID NO: 160)

MRTLFRMIFAIPKFIFRLIWNIIWGIFKTVLVIAIILFGLYYYANHSQSEFANQLS  
DIIQTGKTF

Sequence description

A] Length: 197 bp - 65 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

ID-158

Clone 2-c9

(SEQ ID NO: 161)

ATGTCAAAAAAAAAATAATATTAGGAATTTTATCTCTTTTATCTGTCGTTACTT  
TGGTGGCGTGTGGTTCATCAGACAAACAGCTACAAGATAAAGTTGAGAAA  
AAAGGGAAGTTAGTTTTAGCGGTGAGTCCAGATTATGCTCCCTTTGAGTTT

(SEQ ID NO: 162)

MSKKIILGILSLLSVVTLVACGSSDKQLQDKVEKKGKLVLA VSPDYAPFEF

Sequence description

A] Length: 153 bp - 51 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide (not in frame with nuc)

ID-159

Clone 2-c10

(SEQ ID NO: 163)

5 ATGAAAAATCAAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA  
GGAATACCAGGCAGAACAGAATTTTAAGTCATACTTT

(SEQ ID NO: 164)

10 MKNQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYF

Sequence description

15

A] Length: 139 bp - 46 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

20

ID-160

Clone 2-c11

25

(SEQ ID NO: 165)

ATGATTGGAAAATTATATTATAGCTATAGAAAGTCACGCTTATTAAGAAGT  
ATTTTATGGCTTATTTTAATTGTTGGTGTATATATGTTAGGACAACGTGTTT  
TATTATCCACTGTTTCCTTTATCACATCAAGAGATAAACTAGCAGTAGATC  
30 AACATTTACTCAATAACTTTTCAGCAGTAAGTGGTGGGAGTTTTAATAAAT  
TAAATGTTTTCACACTGGGGTTGAGTCCATGGATGTCAAGTATGATTATTT  
GGAGATTCGTTTCCTTATTTTCGTGGGCAAAAAATGCAACGAAGCGAAAA  
GCAGAAGTAGCTCAATATACTTTAATGCTTACTATCTCAGTTATACAAGCA  
TATGGTGTTCAGGAAATCAATTTATAAAAAGCTCTTTATTAGGTTCTTATA  
35 GTGATATTGTTTTT

(SEQ ID NO: 166)

MIGKLYYSYRKSRLRSILWLILIVGVYMLGQRVLLSTVPLSHQEIKLAVDQHL  
LNNFSAVSGGSFNKLVFTLGLSPWMSSMIIWRFVSLFSWAKNATKRKA-EVA  
40 QYTLMLTISVIQAYGVSGNQFIKSSLLGSYS-DIVF

Sequence description

5 A] Length: 423 bp - 141 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

ID-161

10 Clone 2-c13

(SEQ ID NO: 167)

15 ATGAAAGGTCTATTGGATTTTTTAGTTAATATTGCCAGAACGCCAGCTATT  
TTAGTCGCCTTGATAGCCATTATCGGTTTAGTACTGCAGAAAAAAGGTGTT  
CCTGATATTGTAAAAGGTGGAATAAAAAACATTTGTTGGCTTCTTAGTGGTT  
TCTGAAGGTGCAGGGATAGTCCAAAATTCCTTGAATCCATTTGGAAAAATG  
TTTGAACATGCTTTTCATTTGGTGGGGGTAGTTCCTAATAATGAAGCCATT  
GTAGCAGTAGCTCTTACGAAGTATGGCTCAGCAACTGCTTTGATTATGTTA  
GCGGGAATGATTTTAAATATTTTAATTGCTCGTTTTACAAAA

20

(SEQ ID NO: 168)

MKGLLDFLVNIARTPAILVALIAIIGLVLQKKGVDPDIVKGGIKTFVGFLVVSEG  
AGIVQNSLNPFGKMFHAFHLVGVVPNNEAIVAVALTKEYGSATALIMLAGMI  
FNILIARFTK

25

Sequence description

30 A] Length: 348 bp - 116 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
Shine-Dalgarno sequence. Possible leader  
peptide

35

ID-162

Clone 2-c21

40 (SEQ ID NO: 169)

TTGGTTGGTAAGCCCCAATTACTATTTTTAGATGAACCTACTTCCGGAATG  
GATACTTCCACACGTCAACGATTTTGGGAAGCTGGTTGCGACACTAAAAAA  
AGAAGGTGACACAATTGTCTATTCTAGTCATTATATCGAAGAGGTAGAAC  
ATACAGCTGATAGGATTTTAGTACTTCATAAAGGAAAGTTATTACGCGATA

CAACCCCCTTTGCCATGAAGCAAGAAAAAACCGAAAAGTTATTCACCGTT  
CCGCTTAGTTATCAAAAATTATTACCTACCTATTTGATTACAGAGTGTGAA  
GCCAAGAGTGATAGTATAACGTTTGTACTGGGGAGGCTGAAACTGTATG  
GAAAATACTGGCAGATAATGGTTGTCCTATTGAAGCTATTGAGATGACCA  
5 ATAGAACTTTGTAAATCGTATTTTTGAGACTACTAAGGAGGTAAACATG  
AGAATCTTTA

(SEQ ID NO: 170)

MVGKPQLLFLDEPTSGMDTSTRQRFWKL VATLKKEGDTIVYSSHYIEEVEHTA  
10 DRILVLHKGKLLRDTPFAMKQEKTEKLFTVPLSYQKLLPTYLITECEAKSDSI  
TFVTGEAETVWKILADNGCPIEAIEMTNRTLLNRIFETTKEVKHENL

Sequence description

15

A] Length: 462 bp - 155 aa (partial sequence)  
B] B] Putative TTG start codon is not preceded by  
an obvious Shine-Dalgarno sequence. No obvious  
20 leader peptide. N- and C- termini require further  
examination.

ID-163

25

Clone 2-c25

(SEQ ID NO: 171)

TTGAAAAAATCCAAGAGAAGCCGTAAGGCAGTGACAACAAGTGGTGAGA  
30 AGACTTTACTTGAGGATTTGGCAAAAATGAATTCCTAGACGAAGTCATTA  
ATGTTATGGTTTTATATACCTTGAATAAGACAAAATCTGCTAACTTAAATA  
AGGCCTATATCATGAAAGTTGCTAATGATTTTGCCTTTCAGAATGTTATGA  
CGGCCGAAGATGCTGTGCTTAAAATTCGTGATTTTTTCAGATCAAAAAGTAA  
GGACTAAAACAGAAACGAAGAAGAAACAATCGAATGTTCTGAAATGGAGT  
35 AATCCTGATTATAAAGATGAGGTTAGCCCAGAAAAAGAAATTGAATTAGA  
ACAGTTT

(SEQ ID NO: 172)

MKKSKRSRKAVTTSGEKTLLEDLAKMNFLDEVINVMVLYTLNKTKSANLNK  
40 AYIMKVANDFAFQNVMTAEDAVLKIRDFSDQKVRTKTETKKKQSNVPEWSN  
PDYKDEV SPEKEIELEQF

Sequence description

A] Length:360 bp - 120 aa (partial sequence)  
B] N- and C- termini require verification.

5

ID-164

Clone 2-c28

10

(SEQ ID NO: 173)

ATGACGAATCATATTACTAAACTGATAGAAAATAGCGGAAAAAAATTGAC  
AGAAATTAGCGAAGCTACAGATATAGCCTATCCTACACTTTCTGGATACAA  
TCAAGGAATCCGCAAACCTAAAAAAGATAATGCTGAAAAATTGGCAAAAT  
ACTTTAATGTTTCCGTCGCTTACATTATGGGACTTGATAGCAACCCACATG  
CTCCATCAAATCTT

15

(SEQ ID NO: 174)

MTNHITKLIENSGKKLTEISEATDIA YPTLSGYNQGIRKPKKDNAEKLAKYFNV  
SVAYIMGLDSNP HAPSNL

20

Sequence description

25

A] Length:218 bp - 72 aa (partial sequence)  
B] ATG start codon is preceded by an  
obvious Shine Dalgarno sequence. No obvious  
leader peptide.

30

ID-165

Clone 2-c29

35

(SEQ ID NO: 175)

TTGATGAAAAGGAATAAACATTTACCGTTAACAGAACTACCTATTATATT  
TTATTAGCTTTGTTTGAGGAAGCGCATGGCTATGCTATTATGAAAAAAGTT  
GAAGAAATGAGTGGCGGTGATGTTAGAATAGCCGCAGGGACAATGTACGG  
TGCCATTGAAAATTTACTTAAACAAAAAATGGATAAAGTCTATCTCAAGTGA  
CGATAGAAGAAGAAAAGTTTATATTATTACTGAGACAGGAAAAGAAATAG  
TAGAACTTGAAACGAATCGATTAAGAAAGTTACTTAATACTGCTAATCAGT  
TGGGTTTTTGGAGGAGATGGTTATGATAAAGTTT

40

(SEQ ID NO: 176)

MMKR NKHLPLTETTTYILLALFEEAHGYAIMKKVEEMSGGDVRIAAGTMYG  
AIENLLKQKWIKSISSDDRRRKVYIITETGKEIVELETNRLRKLLNTANQLGFG  
GDGYDKV

5

#### Sequence description

10

A] Length:337 bp - 112 aa (partial sequence)  
B] TTG start codon is preceded by an  
obvious Shine Dalgarno sequence. Actual start  
codon may ATG that comes immediately after the  
TTG. Potential leader peptide.

15

ID-166

Clone 2-c35

20

(SEQ ID NO: 177)

CCCATTACTGGTGAGTTAATAGCTGAGAAATTAGGAGTACCAAGAGCAGC  
ACTAAGGTCTGATTTGCGGGTTTTAAGTATGCTAGGTATCATAGATGCAAA  
ACCTAAGGTTGGTTATTTTTATTTAGGACAGTATCATGCTTCAATAGGGAC  
25 AAGTCATTTTGAAAAGATGACAGTTTCAGAAATTATGGGGATCCTTCTGAC  
AGTTCATCAAAAAGATTTCAGTTTATGATGTTATTGTACATATTTTTATGGA  
AGATGCTGGTTGTGCTTTTATCTTGGATGATGATGATTTTCTCTGTGGAGTC  
GTGTCACGTAAAGATTTACTAAAAACCAGTATTGGCGGAGGAGATCTTTCT  
AAAATGCCAATAGGAATGGTGATGACACGTATGCCACACGTGACAACCTGT  
30 TTTAGAAAATGAAAGTCTTTTTGCGGCAGCTGATAAATTAGTGAGCAGAA  
AAGTGGATAGTCTCCCTGTCGTTTCGTCATGATAAGCAATATCCCGAAAAAT  
TTA

30

(SEQ ID NO: 178)

PITGELIAEKLGVPRALRSDLRVLSMLGIIDAKPKVGYFYLGQYHASIGTSHF  
EKMTVSEIMGILLTVHQKDSVYDVIVHIFMEDAGCAFILDDDDFLCGVVSRKD  
LLKTSIGGGDLSKMPIGMVMTRMPHVTTVLENESLFAAADKLVSARKVDSL PV  
VRHDKQYPEKF

35

40

#### Sequence description

A] Length:511 bp - 170 aa (partial sequence)

B] N- and C-termini to be determined

ID-167

5

Clone 2-44

(SEQ ID NO: 179)

10 TTGGAAGTCATCATGCAATTTATTTATAGTATTATTGGTATTTTATTGGTAT  
TAGGAATTGTGTATGCAATTTCTTTCAATCGTAAGAGTGTCTCTAAGTTT  
AATTGGAAAAGCTCTTATCGTTCAATTCATTATTGCGCTAATCTTAGTACGT  
ATCCCACTAGGCCAACAAAGTTGTTAGTGTTGTTTCAACTGGAGTTACTAAA  
GTAATCAACTGTGGTCAAGCTGGTTT

15 (SEQ ID NO: 180)

MEVIMQFIYSIIIGILLVLGIVY AISFNRSVSLSLIGKALIVQFIILILVRIPLGQQ  
VVSVVSTGVTKVINCGQAG

20 Sequence description

25 A] Length:233 bp - 77 aa (partial sequence)  
B] TTG start codon is preceded by a  
possible Shine Dalgarno sequence. Actual start  
codon may occur further downstream. Potential  
leader peptide.

30 ID-168

Clone 2-46

(SEQ ID NO: 181)

35 CAACCTAATAAAGCTTTAGAAAGTGATGAGATTGATATTAATGCTTTCCAG  
CATTATAATTACTTAACCAATTGGAATAAAGCAAATAAGACCAATCTTGTT  
TCCGTTGCTGAGACATACTTTACTTCCTTTAGATTATACTCTGGTACTAAGA  
ACGGTAAAGGTAAATACCAAACAGTTTCTGAAATTCCAAATAAAGCAACT  
ATTACTATCCCAAACGATGCAGTTAACGAAAGTCGCTCTCTCTACTTGTTA  
40 CAATCAGCAGGCTTGCTAAAATTGAAAGTATCAGGTGATACATTAGCAAC  
AATGTCAGATGTTGTTTCCAATCCTAAATCTTTAGATTT

(SEQ ID NO: 182)

QPNKALESDEIDINAFQHYNLTNWNKANKTNLVSVAETYFTSFRLYSGTKN  
GKGKYQTVSEIPNKATITIPNDVNESRSLYLLQSAGLLKLKVSGDTLATMSD  
VVSNNPKSLD

5

Sequence description

10           A] Length:344 bp - 114 aa (partial sequence)  
              B] N- and C- termini require verification

ID-169

15

Clone 2-47

(SEQ ID NO: 183)

20   ATGAAATGTATAATAAATAATATAAAATAAAAATGATAATTGAGAT  
     TTATCATAGAAGGAAAACCTATTTTGAAATTAAATAAAATCATATTATCTAC  
     TGCAGCTCTTACTGCTCTCTTTTTAGGATATAATAGCGTTACTGCGGATACA  
     TATAATAACTATCAGCCACATAGATCAAATAATATGGATTAACTGAGGA  
25   ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA  
     ATATACCTTTT

25

(SEQ ID NO: 184)

MKCIINNINKIKMIIIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY  
QPHRSNNMDLTEEYNYNQIELQERIKNLNIPF

30

Sequence description

35           A] Length:264 bp - 88 aa (partial sequence)  
              B] There is a Shine-Dalgarno sequence upstream  
                  of this sequence. Potential leader peptide  
                  sequence

40

ID-170

Clone RS-58b



(SEQ ID NO: 185)

TTGGGTGATTATTATGGTAAGAAATATTTTGGTGAGGCAGCTAAAAAAGA  
CGTCGAACATATGGCTAAGAAAATCATTAATGTCTATAAAACACGGTTAA  
5 AAAACAACACTTGGTTATCAGAAAATACAAAAGCAATGGCCATTAAGAAA  
CTTGATAACATGAGATTAATGATTGGCTATCCAGAAGATTATCCTGATCTT  
TATCGTCAGTACCAATTTGATAGTAAAGCAAGCTTCTTTGAAAACAATGAT  
AACTACAGAAAATTATCGAACAAGAAAACATTTGAAGAATTTAACCAGTC  
TAATCAACGTGAACATTGGCAAATGAGTGCCAATGCTGTAAATGCTTATAA  
10 TGATCCTAATACCAATTCCATAGTCTTTCCAGCAGCGATTTTTCAATCACCA  
CTGTACGATAAAACTAAAACAGTTAGTCAAAATTATGGAGCTATCGGAGC  
AATTATTGGTCATGAAATTTCACTCATTTGATATTAATGGTATGAAATA  
TGACGAGAAAGGGAATCTTCACGATTGGTGGACTAAAGAAGATTTAAATC  
ATTATAAGAAATCAACACAAGCTATGATTGACCAATGGGATGGCCTTAA  
GCAGATGGCGGTAAAGTTGATGGTAAATTAACTTTAGCAGAAAATATTGC  
15 AGATAATGGTGGTGTTATGGCATCTCTAGAAGCTCTTAAGACTGAAAAAAT  
CCAACTATAAAGAATTTTTTGAATCATGGGCAAGTATTTGGCGTCAAAAA  
GCAACCAAAGAACAAGTAAGTCCTCAATTCAGTCAGATGTTTCATGCACC  
ATATGAATTGAGAGCTAACATCCCAGTACGTAATTTCCAAGAATTTTATGA  
TGCCTTTGGTGTTAAAAAAGGCGATTCAATGTATCTAAAACCAGAAAAAC  
20 GTTTGACACTTTGGTAA

(SEQ ID NO: 186)

MGDYYGKKYFGEAAKKDVEHMAKKIINVYKTRLKNNTWLSENTKAMAICK  
LDNMRLMIGYPDYPDLRQYQFDSKASFFENNDNYRKLSNKKTFEEFNQSNQ  
25 REHWQMSANAVNAYNDPNTNSIVFPAAIFQSPLYDKTKTVSQNYGAIGAIIGH  
EISHSFDINGMKYDEKGNLHDWWTKEDLNHYKKSTQAMIDQWDGLKADGG  
KVDGKLTLAENIADNGGVMASLEALKTEKIQTIKNFLNHGQVFGVKKQPKNK  
VSPQFSQMFMHMHMN\*

30 Sequence description:

A) Length: 819 bp - 272 aa (full length gene)  
(107 bp of additional DNA sequence (> onwards) is  
35 also included. While not in-frame with the  
described orf, it also shares strong homology  
with the neutral peptidases.

B) This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-89 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-89 gene sequence.  
40 ID-89 and ID-170 together show homology over their combined entire length  
with the neutral endopeptidases from Lactococcus and Lactobacillus. Possesses  
TTG (possible ATG start codon located 13 bp further downstream) start  
codon with no obvious signal peptide. Shine Dalgarno sequence not  
immediately obvious. Possibly located further downstream

ID-171

5 Clone 2-18/22b (Mod2)

(SEQ ID NO: 187)

ATGACCATGATTACGCCAAGCTTCATTAAGGTATCTCTAGATGAAACAAAT  
CGTATGATGCGTATGATATCAGATTTATTAAGTTTATCGCGCATTGATAAT  
10 GAAGTAACGCATTTAGATGTTGAAATGACGAATTTTACAGCTTTCATGACC  
TCAATTTTGAATCGATTTGATCAGATTAGAAATCAAAAAACAGTCACAGG  
AAAAGTTTATGAAATTGTCAGAGATTATCCTCTTAAGTCAATTTGGGTGGA  
AATTGATACAGATAAGATGACTCAAGTGATTGATAACATTTTAAATAATGC  
AGTCAAGTATTCACCAGATGGTGGTAAGATTACAGTTAATCTACGCACAAC  
15 TAAAACGCAGATGATTTTATCAATATCAGACCAAGGCTTAGGTATTCCCAA  
AAAAGATTTACCTCTCATTTTTGATCGTTTTTATCGTGTTGATAAGGCGAGA  
AGTCGTCAACAGGGTGGGACTGGACTTGGTTTGTCAATTGCAAAGAAAT  
TGTTAAGCAGCATAAGGGATTTATTTGGGCTAAGAGTGAGTATGGTAAAG  
GGTCTACTTTTACAATCGTCTTGCCTTATGATAAAGATGCTGTAACCTTATGA  
20 AGAATGGGAGGACGTTGAAGATTAA

(SEQ ID NO: 188)

MTMITPSFIKVSLDETNRMMRMISDLLSLSRIDNEVTHLDVEMTNFTAFMTSIL  
NRFDQIRNQKTVTGKVVEIVRDYPLKSIWVEIDTDKMTQVIDNILNNAVKYSP  
25 DGGKITVNLRTTKTQMILSISDQGLGIPKKDLPLIFDRFYRVDKARSRQQGGTG  
LGLSIAKEIVKQHKGFIAKSEYGKGSTFTIVLPYDKDAVTYEEWEDVED\*

Sequence description:

30 A] Length: 613 bp - 212 aa (full-length gene possibly)  
B] Possible Shine Dalgarno sequence present  
upstream of a ATG start codon. May not have yet  
determined the N- portion of this gene. No  
35 obvious signal peptide.

ID-172

40 Clone 2-54balternate (107b)

(SEQ ID NO: 189)

TTGAAAAAATTATTACTTCTATTCTATTACTTAGTTGCATTTTTTTTATGC  
CAACCATCTCTGCTGAATCTTTTAATGCTTCCGCTAAACATGCCTTAGCAGT

5 TGATTTAGATTTCAGGAAAAATCTTGTATGAAAAAGATGCTAACAAACCCG  
CTGCTATTGCTTCCTTGACTAAAATAATGACCGTTTATATGGTCTATAAAG  
AAATTGATAACGGTAACCTCAAGTGGAATACCAAAGTAAATATATCTGAC  
TACCCTTATCAACTAACACGCGAATCTGATGCTAGTAATGTTTCCTTTAGAA  
10 AAAAGGCGCTATACTGTAAACAACCTCGTGGACGCTGCCATGATTTCTAGT  
GCTAACAGTGCAGCCATTGCTTTAGCTGAACATATTTTCAGGAACTGAAAGT  
AAATTTGTTGATAAAATGACTGCTCAATTGGAAAAGTGGGGAATTCATGAT  
AGCCACCTAGTCAATGCTTCTGGCTTAAATAATAGTATGTTAGGCAATCAC  
ATTTATCCAAAATCGTCACAAAACGACGAAAATAAAAATGAGTGCACGTGA  
15 TATTGCTATTGCTGCCTACCATTGTTGCAACGAATATCCTTCCATTCTTAAG  
ATTACTAGTAAGTCCGTTGCTAAATTTGATAAAGATATTATGCATTCTTAT  
AACTACATGCTACCAGATATGCCTGTCTTTAGACCAGGTATTACAGGTTTG  
AAAAGTGGGACAACGGAATTAGCTGGCCAATCTTTTATTGCTACATCTACT  
GAAAGTGGGAATGAGACTACTCACTGTTATTATGCATGCTGATAAGGCCGAT  
20 AAAGACAAATATGCTCGCTTTACAGCAACTAACTCTCTCTTGAACATATATC  
ACAAACACCTACGAACCTAACCTTGTATTAGCTAAAGGAGCTGCATATAA  
AGGTAAAGAAGCAAGTGTGAGAGACGGAAAAGAACAATCGGTCATCGCT  
GTTGCTAAAAACGATTTGAAAGTAGTACAGAAGAAAAATATCACTAAACA  
AAATCAGTTAAAAATTAACCTTTAAAAAAGAGCTTACTGCTCCTATTACAAA  
25 AAAAGAGAACCTAGGGAAAGCTTATTACGTTGACCTTAATAAGGTTGGAA  
AAGGCTATCTCATAAAGGAACCTAGCGTTCATTTAGTGGCAAAAGATAGT  
ATTGAGCGCAGTTTCTTCCTCAAAGTGTGGTGAATCATTTTGTGCGCTAC  
GTTAACGAAAAACTTTAA

25 (SEQ ID NO: 190)  
MKKIITSILLLSCTFFMPTISAESFNASAKHALAVDLDSGKILYEKDANKPAAIA  
SLTKIMTVYMVYKEIDNGNLKWNTKVNISDYPYQLTRESNASNVPLEKRRT  
VKQLVDAAMISSANSAAIALAEHISGTESKFVDKMTAQLEKWGIHDSHLVNA  
30 SGLNNSMLGNHIYPKSSQNDENKMSARDIAIAAYHLVNEYPSILKITSKSVAKF  
DKDIMHSYNYMLPDMPVFRPGITGLKTGTTELQSFATSTESGMRLTLVIM  
HADKADKDKYARFTATNSLLNYITNTYEPNLVLAKGAAYKGKEASVRDGKE  
QSVIAVAKNDLKVVQKKNITKQNQLKINFKKELTAPITKKENLGKAYYVDLN  
KVGKGYLIKEPSVHLVAKDSIERSFFLVVWNHVFVRYVNEKL\*

35 Sequence description:

A] Length: 1236 bp - 412 aa (full-length gene sequence possibly)

B] A possible Shine-Dalgarno sequence precedes the putative 'TTG' start  
codon. (needs further cloning and sequencing to verify N-terminus)

40

ID-173

Clone 3-60b

(SEQ ID NO: 191)

5 ATGACGCTTCGAGAATTAACAATAGAAGAATTTAAAGAACATTCAGGAAA  
TTATGATTCACAATCATTTTTACAAACACCTGAGATGGCTAAACTTTTAGA  
AAAACGCGGCTATGATGTTAGGTATTTGGGATATCAAGTAGAAAATAAAC  
TAGAGATAATCAGTTTATCTTATATTATGCCAGTCACTGGTGGTTTTCAAAT  
GAAAATTGATTCAGGACCAGTTCATTCAAATTCTAAGTATCTAAAACAATT  
TTATAAAGCATTGCAAGGCTATGCCAAATCCAACGGTGTTCTAGAATTAAT  
10 AGTTGAGCCTTTTGATGATTACCAATTATTCAGTTCGCGGAGTTCCTAGT  
AATCAGGGAAATGATAATCTGATTGAAGATTTTACCAGTTCAGGTTATCAC  
CATGATGGTTTAACAACCTGGTTTTACTGGTAAATATTTATCTTGGCACTATG  
TTAAAAATTTAGAAGGTGTCACCTTCTGAAACGTTACTATCTTCATTCTCTAA  
GACAGGACGAGCTTTGGTTAAGAAAGCAATGTCTTTTGAATCAAGGTTC  
GCGTTCTTAAACGTGATGAGCTACATTTATTTAAAGAGATAACAACCTTCTA  
15 CGTCAAATAGACGTGATTATATGGATAAGTCCTTAGATTATTATCAAGATT  
TTTACGATAGCTTTGAAGGCAAGGCTGAATTTGTGATTGCCACTTTAAATT  
TTAGAGAATACGACCATAACTTGCAAATAAAAGCTGAAGCATTGGAAAAT  
AAGCTT

20

(SEQ ID NO: 192)

MTLRELTIIEEFKEHSGNYDSQSFLQTPEMAKLLEKRGYDVRYLGYQVENKLEI  
ISLSYIMPVTGGFQMKIDSGPVHSNSKYLKQFYKALQGYAKSNGVLELIVEPF  
DDYQLFTSSGVPSNQGNNDNLIEDFTSSGYHHDGLTTGFTGKYLSWHYVKNLE  
25 GVTSETLLSSFSTGRALVKKAMSFGIKVRVLKRDELHLFKEITTSTSNRRDY  
MDKSLDYYQDFYDSFEGKAEFVIATLNFREYDHNLQIKAEALENKL

#### Sequence description

- 30 A) Length: 771 bp - 257 aa (partial gene sequence)  
B) This gene sequence was not identified using the LEEP system. It was  
identified immediately downstream of the ID-65 gene which was identified by  
LEEP, during cloning and sequence analysis of the full-length ID-65 gene  
sequence. Sequence Characteristics:  
35 No obvious leader peptide sequence  
Orf is preceded by a potential Shine-  
Dalgarno sequence.

40 ID-174

Clone 2-17b (ID-80b)

(SEQ ID NO: 193)

TTGTCATTAAGTTTGGTTGCAGTGTTAAATCTTATCCCTCCTAAAATCATGG  
GATCAGTTATTGATGCTATTACAACCTGGAAAATTAACAAGACCACAATTAC  
TATGGAATTTATTAGGTTTGGTTTTGTCAGCTTTAGCTATGTATGGGCTGCG  
5 TATATTTGGCGTATGTATATTTTAGGGACTTCTTACAAATTAGGCCAAGTT  
GTCAGATACCGTTTATTTGAACATTTTACAAAAATGTCTCCTTCTTTTTATC  
AGAAATATCGTACAGGTGATTTAATGGCGCACGCGACCAACGACATCAAT  
TCTCTAACACGTCTTGCAGGAGGAGGAGTTATGTCAGCAGTGGATGCCTCT  
ATCACAGCATTAGTAACGCTTATCACCATGTTCTTTACTATTTTCGTGGCAA  
10 ATGACATTAATTGCGGTTATCCCTTTGCCCTTAATGGCCTTAGCACTAGTA  
AATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCCCTT  
TTCAGAATTAAATAATAAAGTG

(SEQ ID NO: 194)

15 MSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYI  
WRMYILGTSYKLGQVVRYLFEHFTKMSPSFYQKYRTGDLMAHATNDINSLT  
RLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALALVNWGEK  
PMKPSKNLRQPFSELNNKV

20 Sequence description

A) Length: 534 bp - 178 aa (partial gene  
sequence)

25 B) This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-80 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-80 gene sequence.  
Sequence Characteristics:

No obvious leader peptide sequence  
Orf is preceded by a potential Shine-  
Dalgarno sequence.

30

ID-175

Clone 2-11Ab (ID-103b)

35

(SEQ ID NO: 195)

ATGCATATTGAGACTGTTATTGATTTCAAAGAATTAGGAAAAAGATATCGT  
TTTAAAAATCCTACAAAAGAATTAATAGCTGATACTTTAGAACAAGTCTTA  
GAAGTGATAAAAAGAAGTTGATTATTATCAATCTCAAAATTATTATGTTGTT  
40 GGTTATTTATCTTATGAAGCATCTGCTGCTTTTGATTACATTTTAAAGTTT  
CTCAACAGAAGTTGGCTGGGAGAACATCTAGCTTATTTTACAGTACATAAAG  
ATTGTGAGAACGAAGCTTTTCCTTTAAGTTATGAAAATGTTAGATTAGCAG  
ATAATTGGACTGCTAATGTTTCTGAGCAAGAATATCAAGAGGCAATTGCTA

ATATTAAAGGACAAATTAGACAAGGAAATACTTATCAAGTAAATTATACA  
CTAGAGCTTAGCCAACAATTATGCTCGGATCC

(SEQ ID NO: 196)

5 MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYVVG  
LSYEASAAFDSEHFKVSQKLAGHLYFTVHKDCENEAFPLSYENVRLADNW  
TANVSEQEYQEAIANIKGQIRQGNTYQVNYTLELSQQLCSD

10 Sequence description:

A] Length: 440 bp - 146 aa (partial gene sequence)

15 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-103 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-103 gene sequence.  
Shine Dalgarno sequence present upstream of  
ATG start codon, No apparent leader peptide sequence

20 ID-176

Clone 2-18/22b(b) (ID-104b)

(SEQ ID NO: 197)

25 GTGAATAATATGTTTTATCTCAAAATAGCCTGGCATAATTTAAAACATTCT  
ATAGACCAGTACATAACATTCTCTTAGCCAGTTTATTACTTTATTCATTGA  
CTTGTTCTACGCTACTAATCTTAATGAGTGCTGTTGGAAGAGATATGGGGA  
CAGCGGCAACGGTCTTTTTCTTGGAGTGATTGTTTTGTCAATCTTTGCGGT  
AGTCATGGAACATTATAGCTACAATATCTTGATGAAACAGCGTAGTAGTG  
30 AATTTGGACTGTATAACATTTTGGGGATGAATAAACGTCAAGTTGCGCGTG  
TAGCTAGTCTAGAGCTGTTTATTATTTATATATTTCTTATTTCTATAGGAAG  
TCTGTTTAGTGCTTTTTTTTGCTAAATTTATTTATTTAATTTTTGTCAACATTA  
TTAACTATCATGCACTAAATCTTAGTTTAAGTTTATGGCCATTTATTATTTG  
TATCGTTATATTTACAGGTATTTTTCTGACTTTAGAAGTTCCAGTTATTCGA  
35 CATGTTCAATTTATCATCCCCATTAAGTCTTTTTAGAAAGAAACAACAGGGA  
GAAAAAGAACCAAAAGGTAATCTTATACTTGCAATTTTAGCGTTAGTAGCT  
ATCGCCATCGCTTATACAATGGCTCTTACTTCAGGTAAAGCACCTGCATTA  
GCTGTTATCTATCGTTTCTTCTTTGCAGTACTTTTAGTAATTGCTGGTACTT  
ATCTTTTTTATATTAGTTTTATGACATGGTACTTAAAAAGGTTGCGTCAAAA  
40 CAAGCATTATTATTATAAATCTGAGCATTTTGTATCAACTTCGCAAATGAT  
TTTTCGAATGAAGCAAAATGCAGTAGGGTTAGCAAGTATCACTTTATTAGC  
TGTTATGGCTCTAGTTACTATTGCTACAACAGTCTCACTCTATTCAAATACA  
CAAAATGTTGTTACCGGACTATTTCCAAAATCAGTAAGTTTATCAATAGAT  
AATTCAAAAGGTGACGCGAAAAATATATTTGAAGAAAAGATTTTGAAGAA

ACTAGGTAAGTCATCTAAGGAAGCTATCACTTATAATCAGACAATGATTTC  
GATGCCAGTTAGTCAATCAAGTGACTTAATATCACATCTA

(SEQ ID NO: 198)

5 MNNMFYLKIAWHNLKHSIDQYIPFLLASLLLYSLTCSTLLILMSAVGRDMGTA  
ATVLFVLGVIVLSIFAVVMEHYSYNILMKQRSSEFGLYNILGMNKRQVARVASL  
ELFIIYIFLISIGSLFSAFFAKFIYLIFVNIINYHALNLSLSLWPFIIICIVIFTGIFLTLE  
VPVIRHVHLSSPLSLFRKKQQGEKEPKGNLILAILALVAIAIAYTMALTSGKAP  
10 ALAVIYRFFFAVLLVIAGTYLFYISFMTWYLRRLRQNKHYYYKSEHFVSTSQM  
IFRMKQNAVGLASITLLAVMALVTIATTVSLYSNTQNVVTGLFPKSVSLSIDNS  
KGDANKNIFEEKILKKLGKSSKEAITYNQTMISMPVVSQSSDLISHL

Sequence description:

15 A] Length: 1119 bp - 373 aa (partial gene sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-104 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-104 gene sequence.  
20 Possible Shine Dalgarno sequence present  
upstream of a GTG start codon. Possesses a potential  
leader peptide sequence

25 ID-177

Clone 2-5b (ID-112b)

(SEQ ID NO: 199)

30 ATGGTTGAGCCAATTATTTCAATACAAGGACTTCATAAAAAGTTTTGGGAAA  
AATGAGGTTTTAAAAGGCATTGACTTGGATATTCATCAAGGAGAAGTGGT  
GGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTTAAGAACAAT  
GAATCTCTTGGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGATTG  
ATATAACAGACAAAAAGAATGATATTTTTAAAATGCGCGAAAAAATGGGC  
35 ATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAT  
ATTACTTTATCACCTATTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAG  
ACAAAAGCATAACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAA  
TGCTTATCCAGCAAGCTTATCTGGAGGACAACAACACGGATTGCTATTGC  
AAGAGGTCTTGCAATGAATCCTGATGTCCTTCTTTTGTATGAAECTACTTCA  
40 GCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTA  
GCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCA  
CGTGAAGTAGCGGATCGTGTCATTITTATGGATGCAGGGATTATTGTTGAG  
CAAGGGACCCCTAAGAAAGTATTTGAGCAGACAAAAGAAATCCGCACAAG  
AGACTTCTTAAGTAAAGTATTATAA

(SEQ ID NO: 200)

MVEPIISIQGLHKSFSGKNEVLKGIDLDIHQGEVVVIIGPSGSGKSTFLRTMNLLE  
VPTKGTVTFEIDITDKKNDIFKMREKMGMVFQQFNLFNMTVLENITLSPIKT  
5 KGLSKLDAQTKAYELLEKVGLKEKANAYPASLSGGQQORIAIARGLAMNPDV  
LLFDEPTSALDPEMVGEVLTVMQDLAKSGMTMVIVTHEMGFAREVADRVIF  
MDAGIIVEQGTPKKVFEQTKEIRTRDFLSKVL\*

10 Sequence description:

A] Length: 735 bp - 244 aa (full length gene)

15 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-112 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-112 gene sequence.  
Shine-Dalgarno sequence precedes the 'ATG'  
start codon. No obvious leader peptide

20 ID-178

Clone 2-5c (ID-112c)

(SEQ ID NO: 201)

25 ATGTCTCAATATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAAGATATT  
AAGTCAGATTTAGAAGCTATTAAGGAGATGAATCTGAAATTCAGGATCG  
TTTTTACAAAACATTAGAATTTGGAACGGCGGGATTGAGAGGTAAACTTG  
GAGCAGGAACCAATCGTATGAATACTTATATGGTGGGGAAAGCAGCACAA  
GCATTAGCTAATCGATTATTGATCATGGCCCTGAAGCTATTGCACGTGGAA  
30 TTGCAGTTAGTTATGATGTCCCGTTATCAATCTAAGGAATTTGCAGAATTA  
ACTTGGTCCATTATGGCAGCAAATGGTATTAAAGCCTTATATTTA

(SEQ ID NO: 202)

35 MSHMNYKEIYQEWLENDLGLGKDIKSDLEAIKGDSEIQDRFYKTLEFGTAGLR  
GKLGAGTNRMTYMGVGAQAALANRLLIMALKLLHVELQLVMMSRYQSKE  
FAELTWSIMAANGIKALYL

40 Sequence description:

A] Length: 366 bp - 122 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-112 gene which was identified by LEEP,



during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

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ID-179

Clone 2-5d (ID-112d)

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(SEQ ID NO: 203)

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ATGCAACCTGTAAAAGTCGATGAACCTTCTGTTGAAGAAACCATTACTATT  
TTGAAAGGTATCCAAAAAATACGAAGATTATCATCACGTAAAAATATAA  
TAATGATGCCATAGAAGCAGCTGCAGTACTATCTAATCGTTATATCCAAGA  
CCGCTTTTACCTGATAAAGCAATAGACTTATTAGATGAAGCTGGTTCTAA  
AATGAACCTAACACTAAATTTTGTGATCCAAAAGAAATTGATCAACGTCT  
CATTGAAGCAGAAAATTTAAAAGCGCAAGCGACTCGTGAAGAAGATTACG  
AACGTGCAGCTTACTTCCGTGACCAGATTGCAAAATATAAAGAAATGCAG  
CAACAAAAGGTTCGACGATCAAGATACACCTATTATTACCGAAAAACAAT  
TGAGCACATCATTGAAGAAAAAACGAATATCCCTGTTGGTGATTTAAAAG  
AAAAAGAACAATCTCAATTAATTAATCTCGCAGATGACTTGAAACAGCAT  
GTGATCGGCCAGGATGACGCTGTCATTAAGATTGCAAAAGCTATTCGTCGT  
AATCGAGTTGGTCTTGGTAGCCCAAACCGTCCTATTGGTTCCTTTTTATTG  
TAGGACCAACCGGTGTTGGTAAACTGAACTTTCTAAACAAGTAGCAATTG  
AGCTCTTTGGTTCAGCTGATAGTATGATTCGTTTTGATATGTCAGAGTACAT  
GGAAAAGCATGCTGTTGCTAAATTAGTCGGAGCGCCTCCAGGATACGTGG  
GATACGAGGAAGCTGGACAATACTGAAAAGGTTTCGTCGAAATCCTTAC  
TCGCTCATCCTTCTAGATGAAATTGAAAAAGCTCATCCCGATGTCATGCAT  
ATGTTCTTGCAGGTCCTTGATGACGGTCGATTAACAGATGGACAAGGAAG  
AACTGTTAGTTTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTTC  
TGGTAAACTGAAGCAAGTGTTGGCTTTGGTGCCTCACGAGAAGGTAGGA  
CGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCAT  
GCAAGC

(SEQ ID NO: 204)

MQPVKVDEPSVEETITILKGIQKKYEDYHHVKYNND AIEAAVLSNRYIQDRF  
LPDKAIDLLDEAGSKMNLTLNFVDPKEIDQRLIEAENLKAQATREEDYERAAY  
FRDQIAKYKEMQQQKVDDQDTPITEKTIEHIIIEKTNIPVGD LKEKEQSQLINL  
ADDLKQHVIGQDDA VIKIAKAIRNRVGLGSPNRPISFLFVGPTGVGKTELSK  
QLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRR  
NPYSLILLDEIEKAHPDVMHMF LQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGS  
GKTEASVGF GASREGRTNSSSVPGDPLESTCRHAS

Sequence description:

A] Length: 1070 bp ÷ 356 aa (Partial gene sequence)

5 B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

10

ID-180

Clone 2-7b (ID-113b)

15

(SEQ ID NO: 205)

ATGAGAGGGAAGGTTATTTACGGCACAACCCTTATAGGTCTTTTTCTATTC  
TTATTTTTCTATTTTTGGATTCTTAAGCATCACATCGAGAGAATACATCATC  
ATCGTATAAAGCAGGTAGATGCGAAGAGTGATTTAACAGGATTTAAAACC  
CATTGCCCCATTATCAGCATTGATACAAAGCAACAAGTTATTCCTCTTGTT  
20 ACAAAAGAAGGCGGAAAATATGTCAAAGCTAGGGATAATATTAATGTTGA  
TATCGAATTACGGGATTCTCCAAGTAGATCACATCATTATCAGAAAAGCC  
GAGAATTAGGACAAAAGGGTTAATATCATATAGAGGAAATTCCTCTCGTT  
ACTTTGATAAGAAGTCATTGAAAGTTAAGTTTGTTACTAATAAGTTAAAGG  
AAAAGAAGCATCGATTAGCAGGAATGCCTAAAGAATCGGAGTGGGTATTG  
25 CATGGTCCCTTTCTAGACAGAACATTATTAAGAAATTATCTGAGTTATAAT  
ATTGCTGGTGAGATTATGCCTATGCCCCAAACGTTTCGCTACTGTGAGTTAT  
TTGTCAATGGTGAGTATCAGGGAG

30

(SEQ ID NO: 206)

MRGKVIYGTTLIGLFLFLFFYFWIPKHHIERIHHHRIKQVDAKSDLTGFKTHLP  
SIDTKQQVIPLVTKEGGKYVKARDNINVDIELRDSRSHLSEKPRIRTKGLIS  
YRGNSSRYFDKKSLKVKFVTNKLKEKKHRLAGMPKESEWVLHGPFLDRTLLR  
NYLSYNIAGEIMPMPQTFATVSYLSMVSIRE

35

Sequence description:

A] Length: 582 bp - 194 aa (Partial gene sequence)

40 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-113 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-113 gene sequence. ATG start codon is preceded by a Shine-Dalgarno sequence-Possesses a potential leader peptide sequence. C-terminus to be determined.

ID-181

5 Clone 2-17b (ID-117b)

(SEQ ID NO: 207)

CTTCACATTTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCT  
TATTTTAGTGGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATAT  
10 TTTGGGAATCTCTTTTTTTCGCGGTGTTTCTTATAGTATTGTTAGAGATATTC  
GTAGAGATGCTTTTGCTAATATGGAAAGGCTAGGCATGTCTTATTTTGATA  
GGACACCGGCAGGATCTATTGTGTCACGTATTACTAATGATACTGAAGCAA  
TATCTGATATGTTTTTCGGGTATTTTATCAAGTTTATCTCGGCGATATTTAT  
TTTACAGTTACTCTGTACACTATGTTGATGCTAGACATTAACTAACAGG  
15 ACTCGTCGCTCTTTTGTTACCTGTTATCTTTATATTAGTGAATGTCTATCGG  
AAAAAATCAGTCACTGTCATTGCTAAAACGAGAAGTTTACTTAGTGATATC  
AACAGTAAATTATCAGAAAGTATTGAAGGAATTC

(SEQ ID NO: 208)

20 SHFIDHYLTNVNQTA VLILVGYYSMYVLQTLIQYFGNLFARVSYSIVRDIRRD  
AFANMERLGMSYFDRT PAGSIVSRITNDTEAISDMFSGILSSFISAIFFTVTLTYT  
MLMLDIKLTGLVALLPVIFILVNVYRKKSVTVIKTRSLSDINSKLSEIEGI

25 Sequence description:

A] Length: 498 bp - 165 aa (Partial gene sequence)

30 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-117 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-117 gene sequence.  
N- and C-termini have yet to be determined

ID-182

35

Clone 3-8b (ID-120b)

(SEQ ID NO: 209)

40 ATGTACCATATTGAATTAAAAAAGGAAGCTTTACTACCAAGAGAACGCCT-  
AGTTGATTTAGGCGCAGATAGATTGAGTAATCAGGAGTTATTAGCCATTCT  
CTTACGTACAGGTATTAAAGAAAAACCTGTTCTTGAAATTTCAACGCAAAT  
TTAGAAAAACATAAGCAGTTTAGCAGATTTTGGTCAATTATCCTTACAGGA  
GTTGCAATCCATTAAAGGAATCGGTCAGGTAAATCCGTCGAAATAAAAG  
CTATGCTAGAACTAGCAAAACGGATTCACAAAGCTGAATATGATCGTAAA

GAGCAAATTTTAAAGTAGTGAACAATTAGCGAGGAAAATGATGCTCGAATT  
AGGGGATAAAAAACAAGAACATTTAGTAGCTATTTATATGGATACACAAA  
ATCGTATTATCGAACAGAGAACTATTTTTATTGGTACTGTACGTCGTTTCAG  
TAGCAGAGCCAAGAGAAATTCTACATTATGCTTGTA AAAACATGGCAACT  
5 TCTTTGATTATTATACATAATCATCCCTCAGGTTCTCCAAATCCCAGTGAAA  
GTGATTTAAGTTTCACTAAAAAAATAAAACGATCATGTGATCATCTGGGAA  
TTGTCTGCCTAGATCACATCATCGTTGGAAAAATAAATATTATAGTTTTC  
GAGAAGAAGCAGATATTTTATAA

10 (SEQ ID NO: 210)

MYHIELKKEALLPRERLVDLGADRLSNQELLAILLRTGIKEKPVLEISTQILENI  
SSLADFGQLSLQELQSIKGIGQVKSVEIKAMLELAKRIHKA EYDRKEQILSSEQ  
LARKMMLELGDKKQEH LVAIYMDTQNRIIEQRTIFIGTVRRSVAEPREILHYAC  
KNMATSLIIH NHPSGSPNPSES DLSFTKKIKRSCDHLGIVCLDHIIVGKNKYYSF  
15 REEADIL\*

Sequence description:

20 A] Length: 681 bp - 227 aa (full-length gene)

B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-120 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-120 gene sequence.  
ATG start codon is preceded by an typical

25 Shine-Dalgarno sequence. No obvious leader  
peptide sequence

ID-183

30

Clone 3-11b (ID-121b)

(SEQ ID NO: 211)

TGGTTAAAAGTAGTGATAGCTTGTATTCCATCTATTTTAATTGCTTTACCAT  
35 TTGATAATTGGTTTGAAGCTCATTTTAATTTTCATGATTCCGATTGCAATAGC  
CCTAATCTTTTATGGTTTTGTCTTCATATGGGTTGAAAAACGTAATGCACAC  
CTCAAACACAGGTAACCGAATTGGCAAGTATGTCTTACAAGACAGCTTTC  
TTGATTGGATGTTTCCAGGTTCTCAGTATTGTTCCGGGAACCAAGTCGTTCTG  
GAGCTACTATTTTAGGAGCAATTATTATTGGAAGTAGTCGTTCCGGTCGCTG  
40 CTGACTTTACTTTCTTCCTTGCCATCCCAACTATGTTTGGTTATAGTGGACT  
TAAGGCGGTTAAATATTTTTTAGATGGTAACGTCTTGAGTTTAGACCAATC  
TTTAATACTTTTAGTAGCAAGTCTGACAGCTTTCGTAGTTAGTTTATATGTT  
ATTCGTTTCTTGACAGACTATGTCAAACGACACGATTTCACCATCTTTGGT

AAGTATCGTATAGTCTTAGGAAGTTTACTCATCCTCTACTGGTTAGTTG TTC  
ATTTATTCTAA

(SEQ ID NO: 212)

5 WLKVVIACIPSILIALPFDNWFEAHFNFMIPIALIALIFYGFVFIWVEKRNAHLKP  
QVTELASMSYKTAFLIGCFQVLSIVPGTSRSGATILGAIIGTSRSVAADFTFFLA  
IPTMFGYSGLKAVKYFLDGNVLSLDQSLILLVASLTAFVVS LYVIRFLTDYVKR  
HDFTIFGKYRIVLGSLLILYWL VVHLF\*

10

Sequence description:

A] Length: 579 bp - 193 aa (partial sequence)

15 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence  
described in WO 00/06736. N-terminus has yet to be determined.

20 ID-184

Clone 3-11c (ID-121c)

(SEQ ID NO: 213)

25 ATGGAAATGAAACAAATCAGTGAAACAACACTGAAAATTACAATTAGTAT  
GGAAGATTTAGAAAGATCGTGGTATGGAGCTGAAAGATTTCCCTAATCCCTCA  
GGAGAAGACTGAGGAATTTTTCTATTCTGT CATGGATGAATTAGACTTGCC  
AGAAAAC TTTAAAAATAGTGGTATGTTAAGTTTTCGAGTAACACCTAAAA  
AAGATCGCATTGATGTTTTTGTTACAAAGTCTGAATTAAGTAAAGATTTAA  
30 ATTTAGAAGAATTAGCAGATTTGGGTGACATTTCAAAAATGTCTCCAGAAG  
ACTTTTTTAAAACCTTGGAACAATCGATGTTGGAAAAAGGGGATACGGAT  
GCCCATGCCAAATTAGCAGAAATTGAAAATATGATGGATAAAGCAACTCA  
AGAAGTAGTTGAGGAAAATGTTTCTGAAGAACAACCTGAAAAGGAAGTAG  
AAACGATTGGATATGTTCACTATGTCTTTGATTTTGATAATATTGAAGCTGT  
35 AGTTCGATTTTCACAAACGATTGATTTTCCAATAGAAGCTT

(SEQ ID NO: 214)

MEMKQISETTLKITISMEDLEDRGMELKDFLIPQEKTEEFFYSVMDELDPENF  
KNSGMLSFRVTPKKDRIDVFVTKSELSKDLNLEELADLGDISKMSPEDFFKTLE  
40 QSMLEKGD TDAHAKLAEIENMMDKATQEVVEENVSEEQPEKEVETIGYVHY  
VFDFDNIEAVVRFSQTIDFPIEA

Sequence description:

A] Length: 547 bp - 182 aa (Partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-68 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-68 gene sequence. ATG start codon is preceded by an typical Shine-Dalgarno sequence. No obvious potential leader peptide sequence

ID-185

Clone 3-16b (ID-122b)

(SEQ ID NO: 215)

GGAAACCAACGGCCAGTACAATCGTCAAGGGTAGATTATCCTAAACGTAG  
TCGTGCCAAGATTGTAGAAGTTTATTTTAGACAAGCTTCTACTACTGATTA  
TTCTGGTGTTTACAAAGGTTACTATATTGACTTTGAAGCCAAAGAAACCCG  
GCAGAAAACTGCTATGCCTATGAAAAATTTTCATGCTCACCAAATAGAGC  
ACATGGCAAATGTATTACAGCAAAAAGGGATTTGCTTTGTCTTGCTTCATT  
TTTCCACACTTAAGGAAACCTATCTACTCCCTGCTAATGAGTTAATTTTCATT  
TTATCAGATTGATAAAGGCAATAAATCAATGCCTATTGATTATATCAGAAA  
AAATGGATTTTTCGTAAAGGAGAGTGCCTTTCCTCAAGTCCCTTACTTAGA  
TATTATTGAAGAAAAATTATTAGGCGGTGATTACAATTAA

(SEQ ID NO: 216)

GNQRPVQSSRVDYPKRSRAKIVEVYFRQASTTDYSGVYKGYIIDFEAKETRQ  
KTAMPMKNFHAHQIEHMANVLQKKGICFVLLHFSTLKETYLLPANELISFYQI  
DKGNKSMPIDYIRKNGFFVKESAFPQVPYLDIIEKLLGGDYN\*

Sequence description:

A] Length: 447 bp - 149 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-122 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-122 gene sequence. N-terminus has yet to be determined

ID-186

Clone 3-17b (ID-123b)

(SEQ ID NO: 217)

5 GGATCCTAAAAACGCTAAGGTTTATCAAAAAAATGCTGATCAATTTAGTG  
ACAAGGCAATGGCTATTGCAGAGAAGTATAAGCCAAAATTTAAAGCTGCA  
AAGTCTAAATACTTTGTGACTTCACATACAGCATTCTCATACTTAGCTAAG  
CGATACGGATTGACTCAGTTAGGTATTGCAGGTGTCTCAACCGAGCAAGA  
ACCTAGTGCTAAAAAATTAGCCGAAATTCAGGAGTTTGTGAAAACATATA  
AGGTTAAGACTATTTTTGTTGAAGAAGGAGTCTCACCTAAATTAGCTCAAG  
10 CAGTAGCTTCAGCTACTCGAGTTAAAATTGCAAGTTTAAGTCCTTTAGAAG  
CAGTTCCCAAAAACAATAAAGATTACTTAGAAAATTTGGAACTAATCTTA  
AGGTACTTGTCAAATCGTTAAATCAATAG

(SEQ ID NO: 218)

15 DPKNAKVYQKNADQFSDKAMAIAEKYKPKFKAASKYFVTSHTAFSYLAKR  
YGLTQLGIAGVSTEQEPSAKKLAEIQEFVKTYKVTIFVEEGVSPKLAQAVAS  
ATRVKIASLSPLEAVPKNNKDYLENLETNLKVLVKS LNQ\*

Sequence description:

20 A] Length: 433 bp - 144 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-123 gene which was identified by LEEP,  
25 during cloning and sequence analysis of the full-length ID-123 gene sequence.  
N-terminus has yet to be determined

ID-187

30 Clone 3-46/47 (ID-130b)

(SEQ ID NO: 219)

35 ATGAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATACGCCTCAGA  
AACTGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGAGAAATAATTGG  
ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACCTATGCT  
TGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAA  
TGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGATG  
CCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAAAAA  
40 TGAAAGGTATTCAAAAAAAGTGAATTAACAGCAGATAACTCATATTTCT  
AAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCA  
GAAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAACCCC  
ACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGG  
AGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACGTTCTAT  
CTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGC

ACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAA  
AAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGG  
AGAATAA

5 (SEQ ID NO: 220)

MKKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGME  
KADKGTALVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQ  
KTELKQQITHISKVVDLENQLDKFVSGYSEGMKRRLSLAIALLGNPVLILDEP  
TVGIDPSLRRKIWQELINIKDEGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTP  
10 LHLKKQFNVSTIEEVFLKAEGE\*

Sequence description:

15 A] Length: 717 bp - 239 aa (Possible full-length sequence)

B] This gene sequence was not identified using the LEEP system. It was  
identified upstream of the ID-130 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-130 gene sequence. ATG  
start codon is preceded by a possible  
20 Shine-Dalgarno. No obvious potential leader  
peptide sequence

ID-188

25

Clone 3-83b (ID-144b)

(SEQ ID NO: 221)

ATGGTACAAATGATACATGATATGATTAACAATTGAGCATTTTGCTGAG  
30 ACACAAGCTGATTTTCCAGTGTATGATATTTAGGGGAAGTCCATACTTAT  
GGACAACCTTAAAGTAGACTCTGACTCTCTAGCTGCTCATATTGATAGCCTA  
GGCCTTGTTGAAAAATCACCTGTCTTAGTATTCGGTGGTCAAGAATATGAA  
ATGTTGGCGACATTTGTTGCTTTAACAAGTCAGGGCATGCTTATATACCG  
GTTGACCAACACTCTGCTTTGGATAGAATACAGGCTATTATGACAGTTGCT  
35 CAACCAAGCCTTATCATTTCAATTGGTGAATTTCTCTTGAAGTTGATAAT  
GTCCCAATCCTAGACGTTTCTCAAGTTTCAGCTATTTTTGAAGAAAAGACT  
CCTTATGAGGTAACACATTCTGTTAAAGGTGATGATAATTACTATATTATT  
TTCACCTCAGGGACTACTGGTTTACCAAAAGGTGTGCAAATTTACATGAC  
AATTTATTGAGCTTACAAATTGGATGATTTCTGATGATGAGTTTCAGTTC  
40 CTGAAAGACCGCAAATGTTGGCTCAACCC

(SEQ ID NO: 222)

MVQMIHDMIKTIEHFAETQADFPVYDILGEVHTYQQLKVSDSLAAHIDSLGL  
VEKSPVLVFGGQEYEMLATFVALTKSGHAYIPVDQHSALDRIQAIMTVAQPSL



IISIGEFPLEVDNVPILDVSQVSAIFEEKTPYEVTHSVKGDDNYIIFTSGTTGLP  
KGVQISHDNLLSFTNWMISDDEFSVPERPQMLAQP

5      Sequence description:

- A] Length: 592 bp - 197 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
10      identified downstream of the ID-144 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-144 gene sequence.  
Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No obvious  
leader peptide sequence  
15      This orf is not in frame with nuc

ID-189

20      Clone 3-86b (ID-145b)

(SEQ ID NO: 223)  
ATGGAATAATCATCGTTATGAAGATGAAGGTAAATTCCAGCGTAAGATGAC  
CAGTCGTCATCTCTTTATGTTATCGCTAGGTGGTGTATCGGGACTGGGCTT  
25      TTCTTGAGTTCAGGTTATACCATGTCACAGGCTGGTCCGCTTGGAGCTGTG  
CTGTCTTATTTGATTGGTGCCGTTGTGGTTTATTTGGTCATGCTATCACTTG  
GGGAATTGGCGGTTGCCATGCCGGTGACGGGGTCATTCCACACTTATGCCA  
CTAAGTTTATCAGTCCTGGAACAGGTTTTACTGTTGCTTGGCTATATTGGAT  
TTGTTGGACGGTCGCCTTGGGGACTGAATTTTTAGGTGCTGCCATGCTGAT  
30      GCAGCGCTGGTTCCCAAATGTGCCGGCTTGGGCATTTGCTTCCTTTTTTGCC  
CTTGTGATTTTTGGTTTAAATGCTCTTAGCGTACGCTTTTTTGCAGAAGCAG  
AGTCTTTCTTCTCAAGTATTAAGGTTATTGCTATCATTATCTTTATTATCTTG  
GGCTTAGGTGCTATGTTTGGTCTAGTTTCCTTTGAAGGTCAGCACAAAGGCT  
ATTCTCTTCACTCATCTGACTGCCAATGGTGCCTTTCCAAATGGTATCGTTG  
35      CAGTTGTCTCAGTCATGTTGGCTGTAACTATGCCTTCTCTGGTACTGAGTT  
AATTGGTATTGCGGCTGGTGAAACGGATAATCCCAAAGAAGCTGTACCAA  
GGGCTATTAAAACGACAATCGGTCGCTTGGTTGTTTTCTTTGTAAGTACAA  
TTGTTGTCCTAGCTTCGCTATTGCCAATGAAAGAGGCAGGCGTATCCACAG  
CACCATTTCGTTGATGTCTTTGACAAGATGGGAATCCCTTTACGGGEGGATA  
40      TCATGAACCTTCGTTATCTTGACAGCCATCCTGTCTGCTGGTAACTCAGGTCT  
CTACGCATCAAGCCGTATGCTCTGGTCCCTTGCCAATGAAGGTATGTTGTC  
AAAATCTGTTGTGAAAATCAATAAACACGGTGTCCCAATGCGTGCTCTTCT  
CTTGTCAATGGCAGGAGCAGTGCTGTCGCTCTTTTCAAGTATTTACGCTGC

AGACACAGTTTATCTAGCCTTGGTTTCAATCGCGGGCTTTGCTGTTGTTGTC  
GTATGGCTAGCCATTCCAGTCGCACAAATCAATTTCCGCAAGGAATTC

(SEQ ID NO: 224)

5 MENHRYEDEGKFQRKMTSRHLFMLS LGGVIGTGLFLSSGYTIAQAGPLGAVL  
SYLIGAVVVYLVMLS LGELAVAMPVTGSFHTYATKFISPGTGFTVAWLYWIC  
WTVALGTEFLGAAML MQRWFPNVP AWAFASFFALVIFGLNALS VRFFAEAES  
FFSSIKVIAIIIFILGLGAMFGLVSFEGQHKAILFTHLTANGAFPNGIVAVVSVM  
10 LAVNYAFSGTELIGIAAGETDNPKEAVPRAIKTTIGRLV VFFVLTIVVLASLLPM  
KEAGVSTAPFVDVFDKMGIPFTADIMNFVILTAILSAGNSGLYASSRMLWSLA  
NEGMLSKSVVKINKHGVPMRALLSMAGAVLSL FSSIYAADTVYLALVSIAGF  
AVVVVWLAIPVAQINFRKEF

15 Sequence description:

A] Length: 1126 bp - 393 aa (partial gene  
sequence)

20 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-145 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-145 gene sequence.  
Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
25 possible leader peptide sequence.

ID-190

30 Clone 3-94b

(SEQ ID NO: 225)

TCAGAAAATGCAGAGGCAGCAACGGTTGCCACAACTTGGTTACCAAAGG  
AGCTAATGTCATTATCGGACCAGCAACATCGGGTGCAGCTGCATCTTCAAC  
35 TCCAAAAGTAAATGCAGCAGCAGTTCCAATGATTGCACCTGCTGCGACAC  
AAGACAATTTAGTCTATGGTTCTGATGGAAAAACCTTAAATCAGTATTTCT  
TCCGAGCTACTTTTGTGCGATAATTATCAAGGAAAGCTATTGTCTCAGTATG  
CTACAGACAACCTTAAAGCTAAAAAAGTTGTTCTATTTTATGATAATTCAT  
CAGATTACTCAAAGGGGGTAGCAAAATCATTTAAGGAAAGTTATAGTGGA  
40 AAAATTGTTGATAGTATGACATTCTCCGCTGGTGATACTGATTTCCAAGCG  
TCATTGACTAAGTTGAAAGGGAAAGAATATGATGCTATTGTGATGCCAGG  
TACTATACCGAGACAGGATTAATAGTTAAGCAAGCGCGTGATTTAGGTAT  
CTCTAAACCGGTTCTTGGGCCTGATGGTTTTGATAGTCCGAAATTTGTGCA

ATCGGCAACACCTGTAGGAGCTTCAAACGTTTATTATTTGACAGGTTTCAC  
TACACAAGGATCAACCAAAGCTAAAGCT

(SEQ ID NO: 226)

5 SENAEAATVATNLVTKGANVIIGPATSGAAASSTPKVNAAAVPMIAPAATQD  
NLVYGSDGKTLNQYFFRATFVDNYQGKLLSQYATDNLKAKKVVLFYDNSSD  
YSKGVAKSFKESYSGKIVDSMTFSAGDTDFQASLTKLKGKEYDAIVMPGYT  
ETGLIVKQARDLGISKPVLGPDGFDSPKFVQSATPVGASNVYYLTGFTTQGST  
KAKA

10

Sequence description

15

A] Length: 637 bp - 231 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-149 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-149 gene sequence. N- and C-termini have yet to be determined

20

ID-191

Clone 2-c94b (ID-153b)

25

(SEQ ID NO: 227)

TTGGGACTTAAAGACCATGCTTTAGTCTATCCATTTTCATTATCTGGGGGG  
CAAAAGCAACGTGTCGCACTAGCTCGTGCGATGATGATTGATCCACAGATT  
ATTGGTTATGATGAGCCAACTAGCGCTCTTGATCCAGAGTTGCGTCAAGAA  
30 GTAGAAAAACTAATTTTACAAAATAGAGAAACAGGTATGACACAAATTGT  
AGTAACACATGATCTTCAATTTGCTGAAAGTATATCTGATACGATTCTCAA  
AATTAATCCTAAGTAG

30

(SEQ ID NO: 228)

35

MGLKDHALVYPFSLSGGQKQRVALARAMMIDPQIIGYDEPTSALDPELRQEV  
EKLILQNRETGMTQIVVTHDLQFAESISDTILKINPK\*

Sequence description

40

A] Length: 270 bp - 90 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-153 gene which was identified by LEEP, during cloning and sequence analysis of the ID-153 gene sequence.  
N-terminus has yet to be determined

5

ID-192

Clone 2-c1b (ID-155b)

10

(SEQ ID NO: 229)

ATGACTAATATCTCAGATGTTCCAAAAGCTATTAGAACACAGGCACAGTAT  
GTTCTCTTGGAATGAGAGTTATGGATCAGTCGGTATTACCGAAAACATAT  
AATTCAAAAGAACCCTTATTTGAAACCAGATATGATTTATATTCATGATAGA  
15 AGACAAGAGACAATGCTTAAAATCACTCAAGAAATAGAAATGGAGCATTG  
A

(SEQ ID NO: 230)

MTNISDVPKAIRTQAQYVLLGMRVMDQSVLPKTYNSKEPYLKPDMIYIHDRR  
20 QETMLKITQEIMEH\*

Sequence description

25

A] Length: 204 bp - 68 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-155 gene which was identified by LEEP, during cloning and sequence analysis of the ID-155 gene sequence.

30

ATG start codon is preceded by a potential typical Shine-Dalgarno sequence.  
Has a  
typical leader peptide. N-terminus has yet to be  
verified

35

ID-193

Clone 2-54altb (ID-172b)

40

(SEQ ID NO: 231)

AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCTTGGGGAATATAAATT  
TGGATTTTCATGACGATGTAAAGCCAATTTATTCTACGGGAAAAGGTCTAAA  
TGAGGCTGTTATTCGTGAGTTATCTGCAGCTAAGGGTGAACCTGAGTGGAT  
GTTGGACTTTCGTCTAAAATCCTTGGAACGTTTAATAAAAATGCCGATGCA

5 GACCTGGGGAGCAGATTTATCAGATATTGATTTTGATGATATTATTTATTA  
 TCAAAAAGCATCTGATAAACCTGCGCGTGATTGGGATGATGTTCCAGAAA  
 AAATCAAAGAACTTTTGAAAGAATTGGGATTCCAGAAGCTGAAAGAGCC  
 TATCTTGCAGGAGCATCAGCACAATATGAATCAGAAGTAGTTTATCACAAT  
 10 ATGAAAGAAGAATATGATAAGCTGGGTATTGTTTTTACGGATACTGACTCT  
 GCACTTAAAGAGTACCCAGAGCTATTCAAAAAATATTTTGCTAAACTTGTC  
 CCTCCAACAGATAATAAATTAGCTGCTCTGAACTCTGCTGTATGGTCAGGT  
 GGAACATTTATTTATGTTCCCTAAAGGTGTTAAGGTGGATATTCCACTTCAA  
 ACTTACTTCCGTATTAATAATGAAAATACTGGACAATTTGAACGTACTCTC  
 ATTATTGTTGATGAGGGAGCAAGTGTTCACTATGTTGAAGGTTGTACCGCC  
 CCAACTTATTCTTCAAATAGTTTACATGCAGCTATAGTTGAAATTTTTGCAC  
 TTGATGGAGCTTATATGCGCTATACGACTATTCAAAATTGGTCCGATAATG  
 TCTATAATTTAGTGACAAAACGTGCTACCGCTAAAAAAGATGCAACAGTT  
 15 GAGTGGATAGATGGAAATCTAGGAGCTAAAACAACAATGAAATACCCATC  
 GGTTTACCTTGATGGTGAAGGAGCACGTGGCACGATGTTGTCTATTGCTTT  
 TGCAAACAAAGGACAACACCAAGATACGGGTGCAAAGATGATTCATAATG  
 CCCCCATACTAGTTCATCCATTGTCTCTAAATCAATTGCTAAGGGTGGGG  
 GAAAAGTTGATTATCGAGGTCAAGTGACATTTAATAAAGATTCCAAAAAA  
 TCAGTGTACATATAGAATGTGACACCATATTGATGGATGATATTTCAAAA  
 20 TCAGATACCATAACCGTTTAATGAGATTCATAATTCACAGGTTGCTTTAGAG  
 CATGAAGCAAAGGTGTCTAAGATTTCTGAAGAGCAACTGTACTACTTGATG  
 AGTCGAGGTTTATCTGAAGCTGAAGCAACAGAAATGATTGTTATGGGGTTT  
 GTTGAGCCCTTTACGAAAGAATTACCAATGGAATATGCGGTAGAGTTAAA  
 TCGTTTAATTCCTATGAAATGGAAGGTTTCAGTTGGTTAA

25

(SEQ ID NO: 232)

30 MHACRSTLEDLGEYKFGFHDDVKPIYSTGKGLNEAVIRELSAAKGEPEWMLD  
 FRLKSLETFNKMPMQTWGADLSIDFDDIYYQKASDKPARDWDDVPEKIKE  
 TFERIGIPEAERAYLAGASAQYESEVVYHNMKEEYDKLGIVFTDSDSALKEYP  
 ELFKKYFAKLVPPTDNKLAALNSAVWSSGTFIYVPKGVKVDIPLQTYFRINNE  
 NTGQFERTLIIVDEGASVHYVEGCTAPTYSSNSLHAAIVEIFALDGAYMRYTTI  
 QNWSDNVYNLVTKRATAKKDATVEWIDGNLGAKTMMKYPSVYLDGEGARG  
 TMLSIAFANKGQHQDTGAKMIHNAPHTSSSIVSKSIKGGGKVDYRGQVTFN  
 35 KDSKKSVSHECDTILMDDISKSDTIPFNEIHNSQVALEHEAKVSKISEEQLYYL  
 MSRGLSEAEATEMIVMGFVEPFTKELPMEYAVELNRLISYEMEGSVG\*

Sequence description:

40

A] Length: 1411 bp - 469 aa (Possible full-length gene)

B] This gene sequence was not identified using the LEEP system. It was  
 identified downstream of the ID-72 gene which was identified by LEEP,  
 during cloning and sequence analysis of the full-length ID-72 gene sequence.  
 No obvious Shine Dalgarno sequence upstream of

TTG start codon insufficient sequence data). N terminus needs verification.

5 ID-194

Clone 3-1b (ID-81b)

(SEQ ID NO: 233)

10 ATGATAGAATTCTTTTCTAATATCAGAACAGAGATTCCGCAGATGCCTTTA  
CTTATCCATAGTTTGATTTTATCTGTCTTACCTTTTCTGATGTGGCTGACTTT  
GGTTAATAGAGATAAGCCTTTGTATAAACTATTTGGAGTATCCTTTTAGG  
ACTTCAGTTAATTACGATTTATACTTGGTTTTTCTGGGCAAAATTGCCTTTA  
15 TCTGAAAGTCTTCCCCTTTACCATTGTCTGAATAGGCATGTTTGTCTGGTCTCT  
TA

(SEQ ID NO: 234)

MIEFFSNIRTEIPQMPLLIHSLILSVLPFLMWLTLVNRDKPLYKTIWSILLGLQLI  
20 TIYTWFFWAKLPLSESLPLYHCRIGMFVGLL

Sequence description

A) Length: 261 bp - 87 aa (partial gene sequence)

25 B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-81 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-81 gene sequence. Sequence Characteristics: Possesses a potential leader peptide sequence Orf is preceded by a potential Shine-Dalgarno sequence.

30 ID-195

Clone RS-55b

35 (SEQ ID NO: 235)

AAGCTTGTGCAAAGTATTAAGAGATAGGATTAGCTAATGCGCATTATTATTA  
GCTGTTGCTCCGACAGGGTCAATCAGTTATCTTTCTTCTTGTACTCCGAGCC  
TTCAACCGGTTGTATCACCTGTCGAAGTACGCAAGGAAGGAGCACTGGGG  
AGGGTTTATGTAGCTGCTTATAAGATTGATGCAGATAATTATGTCTAETAC  
40 AAAAAAGGAGCTTATGAAGTGGGATCTGAGGCGATTATCAATATTGCAGC  
TGCCGCTCAAAAACACATTGATCAAGCTATTTTCGTAAACGCTTTTCATGAC  
AGATCAAGCAACTACGCGAGATTTAAATAAAGCCTATATTCAAGCATTTA  
AACAAAAATGTGCCTCTATTTATTATGTACGAGTGAGACAGGACATCCTAG

AAGGTAGCGAGAGTTATGATGATATGCTGGATGATTTCACTTCATCGGACT  
TAGAAGACTGTCAATCCTGCATGATTTAA

(SEQ ID NO: 236)

5 KLVQSIKEIGLANAHLAVAPTGSISYLSCTPSLQPVVSPVEVRKEGALGRVY  
VAAYKIDADNYVYYKKGAYEVGSEAIINIAAAAQKHIDQAISLTLFMTDQATT  
RDLNKAYIQAFKQKCASIYYVRVRQDILEGSESYDDMLDDFTSSDLEDCQSC  
MI\*

10

Sequence description:

A] Length 486 bp - 162 aa (Partial sequence)

15 B] This gene sequence was not identified using the LEEP system. It was identified  
upstream of the ID-87 gene which was identified by LEEP, during cloning and  
sequence analysis of the full-length ID-87 gene sequence. N-terminus to be  
determined.

20

ID-196

Clone RS-59(ID-90b)

(SEQ ID NO: 237)

25 GTGAGGACATATATTACAAACTTGAATGGACATTCAATCACTAGTACAGC  
ACAAATAGCTCAAAACATGGTAACAGATATAGCAGTAAGCTTAGGTTTTTC  
GTGAGCTGGGAATACATTCTTATCCGATTGATACTGATTCTCCTGAGGAAA  
TGAGTAAGCGTTTAGATGGAATCTGTTCCGGACTIONAGAAAAAATGATATTG  
TCATATTTTCAGACACCTACATGGAACACTACAACTTTTGATGAAAAATTAT  
30 TTCACAAATTAAAAATATTTGGTGTAAGATTGTTATTTTTATACATGATGT  
TGTACCGCTAATGTTTGATGGAAATTTTTATTTGATGGATAGAACTATAGC  
TTATTATAATGAAGCAGATGTTTAATAGCCCCTAGTCAAGCAATGGTCGAT  
AAGCTT

35

(SEQ ID NO: 238)

MRTYITNLNGHSITSTAQIAQNMVTDIAVSLGFRELGIHSYPIDTDSPEEMSKRL  
DGICSGLRKNDIVIFQTPTWNTTTFDEKLFHKLKIFGVKIVIFIHDVVPLMFDGN  
FYLMDRITIAYYNEADVLIAPSQAMVDKL

40

Sequence description:

A] Length: 414 bp - 138 aa(partial gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence. No obvious signal peptide, but a possible Shine Dalgarno sequence is present upstream of ATG start codon. C-terminus has yet to be determined.

10 ID-197

Clone RS-59c (ID-90c)

(SEQ ID NO: 239)

15 CATGGAAATGAAGTTGATGATGTTATTAGAAGGGCATTGGAATATAATCAC  
CTTATCTTTGCTTTTGATAATACCTGTCATAACAGAGAGTTAGTATTAGATA  
GCAATATCATTTCTCACACAACCTGTGAACAATTGATAAATTTAATGAAAA  
ATTTATCAGGCTCCATTATGTATTTGCTAGAGCAACAAAGAGAACAACA  
20 AGTAATGAAACAAAAGAGCGTTATAAAGAAATATTAGGAGGGTATGGAA  
ATGCCTAA

(SEQ ID NO: 240)

HGNEVDDVIRRAFEYNHLIFAFDNTCHNRELVLDSNIISHTTCEQLINLMKNLS  
25 GSIMYLLEQQREQTSNETKERYKEILGGYGNA\*

Sequence description:

A] Length: 261 bp - 87 aa(partial gene sequence)

30 B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence. N-terminus has yet to be determined

35

ID-198

Clone RS-70b (ID-93b)

40 (SEQ ID NO: 241)

ACATTTTTATATTATGTATTTGAAGACGTAGCCACCCAGTCAAATATGACT  
GGGAAGATTTTGTAGTATGTCTAAAGAAGAGTTGTCATATTTACCCGTTATT  
AAACTTTTAAAGAATCAAGGTGTATACAACGGCTTGATTGGTCTATTCCTC  
CTTTATGGGTATATATTTTACAGAATCAAGAAATTGTAGCTATTTTTTTAA



TCAATGTGTTGCTAGTTGCTGTTTATGGTGCTTTGACAGTTGATAAAAAAA  
TCTTATTAAAACAGGGTGGTTTACCTATATTAGCTCTTTTAACATTCTTATT  
TTAA

5 (SEQ ID NO: 242)

TFLYYVFEDVATQSNMTGKIFSMSKEELSYLPVIKLFKNQGVYNGLIGLFLLY  
GLYSISQNQEIVAIFLINVLLVAVYGALTVDKKILLKQGGLPILALLTFLF\*

10 Sequence description:

A] Length: 312 bp - 104 aa (partial gene sequence)

15 B] This gene sequence was not identified using the LEEP system. It  
was identified upstream of the ID-93 gene which was identified by  
LEEP, during cloning and sequence analysis of the full-length ID-93  
gene sequence.

N-terminus has yet to be determined

20 ID-199

Clone RS-70c (ID-93c)

(SEQ ID NO: 243)

25 ATGAAATTAAGTGTCTTGATTATGGGCTTATTGATTATGGAAAACTGCA  
AGTGATGCAATACAAGAAACGATTCTTTTATCACAAGAGGCGGAGCAACT  
AGGCTATCATCAATTTTGGGTGGCTGAACATCACGGTGTTAAGGCATTTCAG  
TATTAGCAATCCAGAATTAATGATAATGCATTTGGCTAACCAGACTAAATC  
TATCAAAATTGGCTCTGGAGGTATAATGCCTCTGCACTATAGTAGTTTTAA  
30 ACTCGCGGAGACTCTCAAGACATTAGAGACATGTCATCCGAATCGAGTAA  
GTATTGGTTTAGGAAATTCAGTAGGGACAGTTAAAGTTTCAAATGCACTTC  
GTAGCTTACATAAAGCACATGATTACGAAGAGGTACTGGAGGAATTGAAG  
TCATGGCTTATTGATGAATCATCCAGTAAGGAACCATTAGTTCAACCGACT  
CTTTCTAGCTTCCCAGACTTATATGTGTTGGGGAGTGGTCAAAAATCAGCT  
35 TATTTAGCGGCTAAACTTGGCTTAGGCTTTACCTTCGGTGTTTTTCTTTTA  
TGGACAAAGACCCATTGACAGAAGCTAAA

(SEQ ID NO: 244)

40 MKLSVLDYGLIDYGKTASDAIQETILLSQEAEQLGYHQFWVAEHHGVKAFFSIS  
NPELMIMHLANQTKSIKIGSGGIMPLHYSSFKLAETLKTLETCHPNRVSIGLGN  
SLGTVKVSNALRSLHKAHDYEEVLEELKSWLIDESSSKEPLVQPTLSSFPDLYV  
LGSGQKSAYLAACLGLGFTFGVFPFMDKDPLEAK

Sequence description:

- 5           A] Length: 588 bp - 196 aa (partial)  
           B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence. No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.

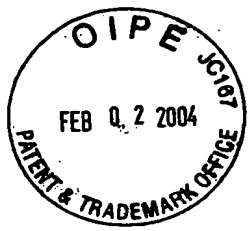
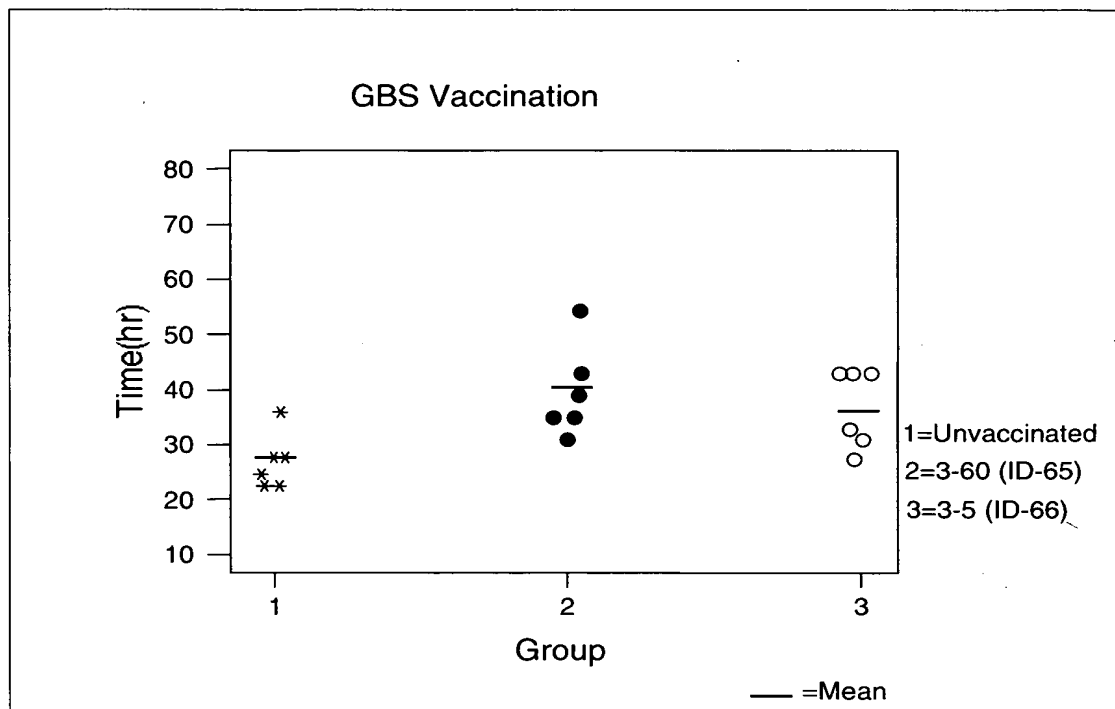


Figure 2



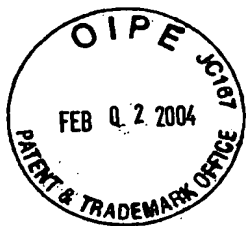


Figure 3

nucS1

Bgl II Eco RV

5'-cgagatcttgatatctcacaacagataacggcgtaaatag -3' (SEQ ID NO.: 245)

nucS2

Bgl II Sma I

5'-gaagatcttcccccggatcacaaacagataacggcgtaaatag -3' (SEQ ID NO.: 246)

nucS3

Bgl II Eco RV

5'-cgagatcttgatatccatcacaaacagataacggcgtaaatag -3' (SEQ ID NO.: 247)

nucR

Ban HI

5'-cgggatccttatggacctgaatoagcgttgto -3' (SEQ ID NO.: 248)

NucSeq

5'-ggatgccttgtttcaggtgtato -3' (SEQ ID NO.: 249)

pTREP<sub>F</sub>

5'-catgatatcggtacctcaagctcatatcattgtccggcaatggtgtgggcttttttgttttagcggataa  
caatttcacac -3' (SEQ ID NO.: 250)

pTREP<sub>R</sub>

5'-gaggatcccccggttaattaatgtttaaacactagtcgaagatctcgcgaattctcctgtgtgaaatt  
gttatccgcta -3' (SEQ ID NO.: 251)

pUC<sub>F</sub>

5'-cgccagggttttcccagtcacgac -3' (SEQ ID NO.: 252)

V<sub>R</sub>

5'-tcaggggggaggagcctatg -3' (SEQ ID NO.: 253)

V<sub>1</sub>

5'-tcgtatgttggtggaattgtg -3' (SEQ ID NO.: 254)

V<sub>2</sub>

5'-tccggctcgatgttggtggaattg -3' (SEQ ID NO.: 255)

Figure 4

pTREP-Nuc vectors allow cloning of genomic DNA into each frame with respect to the nuclease gene

5

(i)

pTREP1-nuc1 (EcoRV)	AAGTATCAGATCT-- <u>GATATC</u> --TCACAAACAGATAACGGCGTAAAT	Frame+1
(SEQ ID NO.:256)	.....▲.....	
pTREP1-nuc2 (Sma I)	AAGTATCAGATCTT <u>CCCGGCA</u> --TCACAAACAGATAACGGCGTAAAT	Frame+2
(SEQ ID NO.: 257)	.....▲.....	
pTREP1-nuc3 (EcoRV)	AAGTATCAGATCT-- <u>GATATC</u> CAACAGATAACGGCGTAAAT	Frame+3
(SEQ ID NO. 258)	.....▲.....	
Nuclease Gene	TCACAAACAGATAACGGCGTAAAT	
	(SEQ ID NO.: 259)	

Cloning site is indicated by an arrow

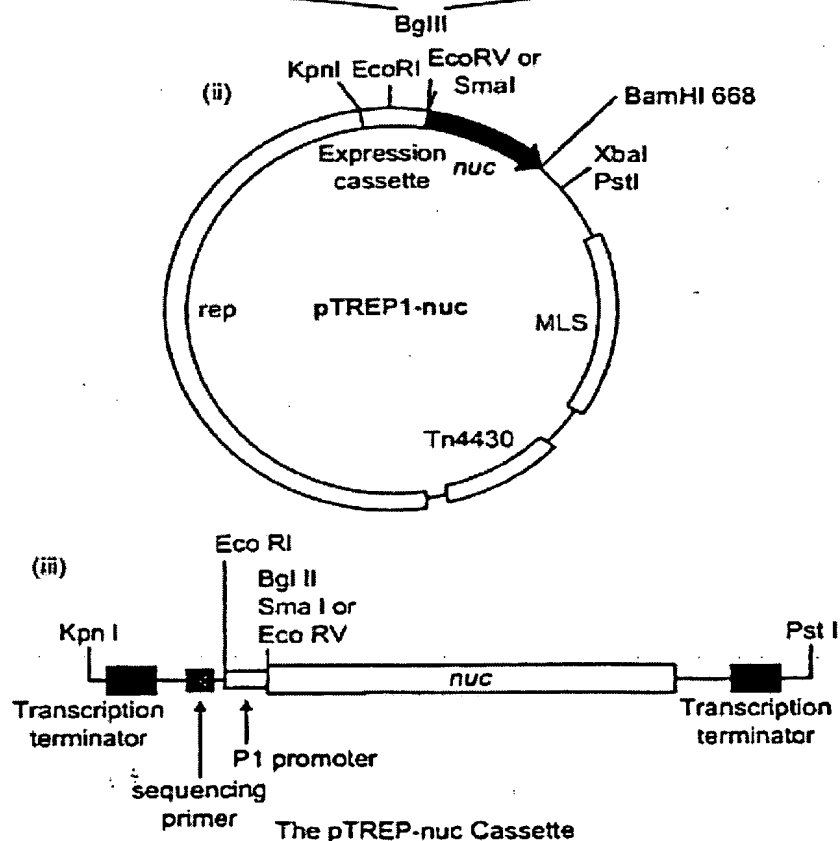




Figure 5

SDS-PAGE analysis of the purified ID-65 and ID-83 protein antigens

5

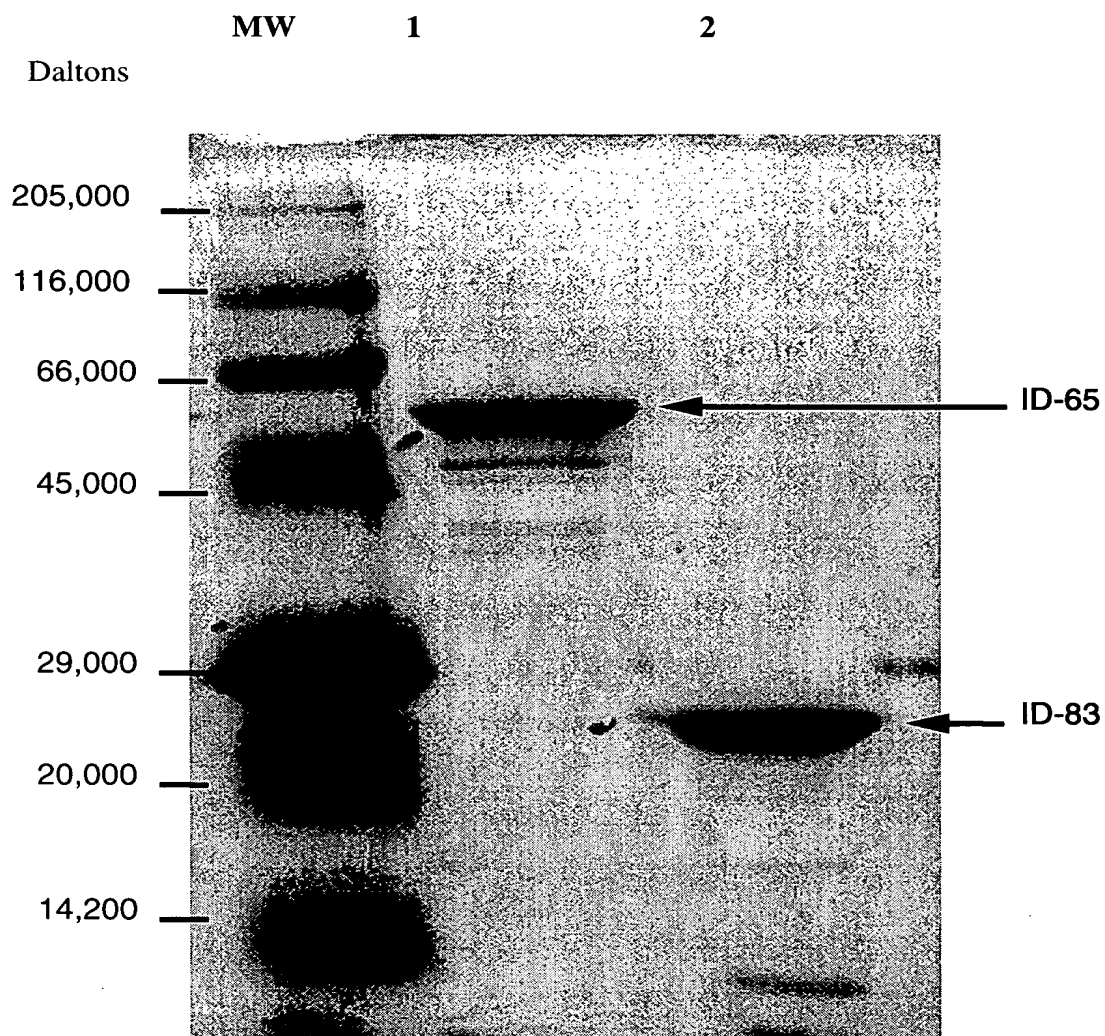
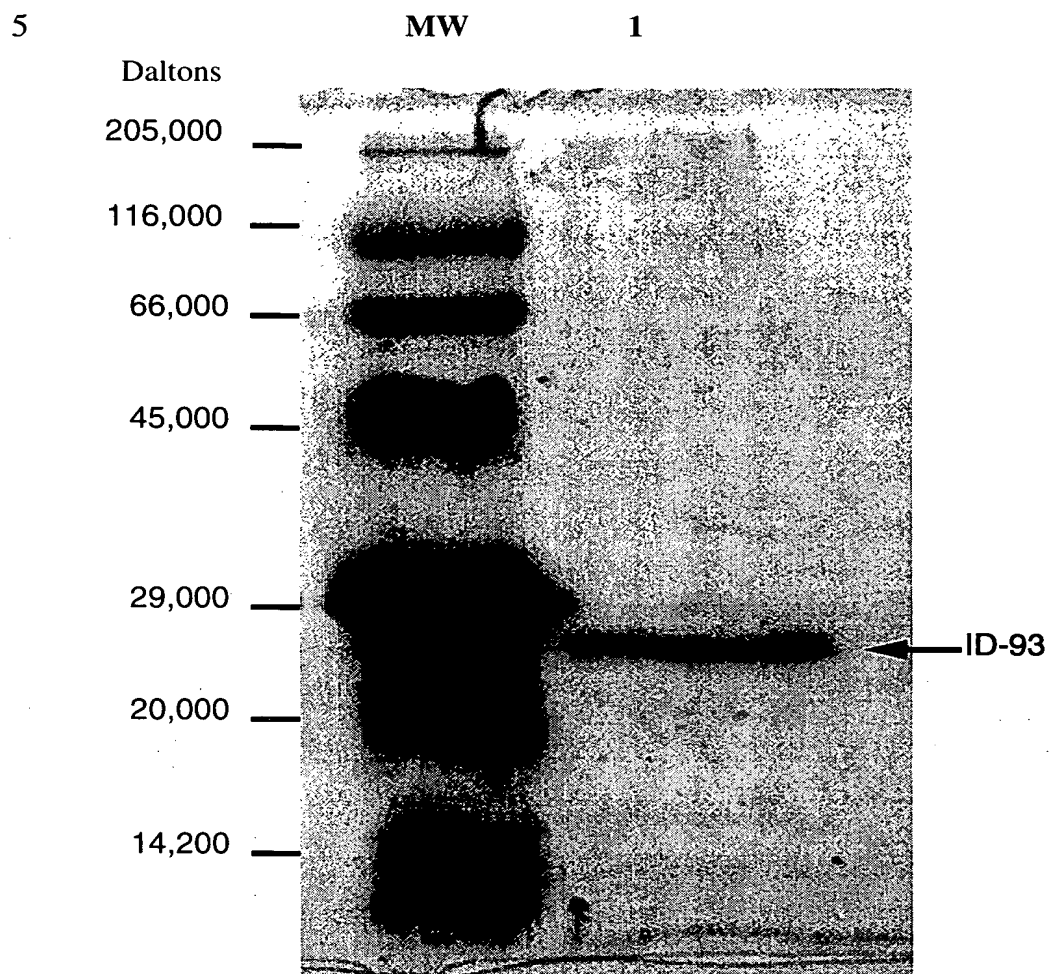




Figure 6

SDS-PAGE analysis of the purified ID-93 antigen



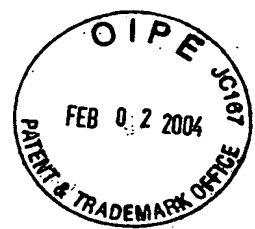
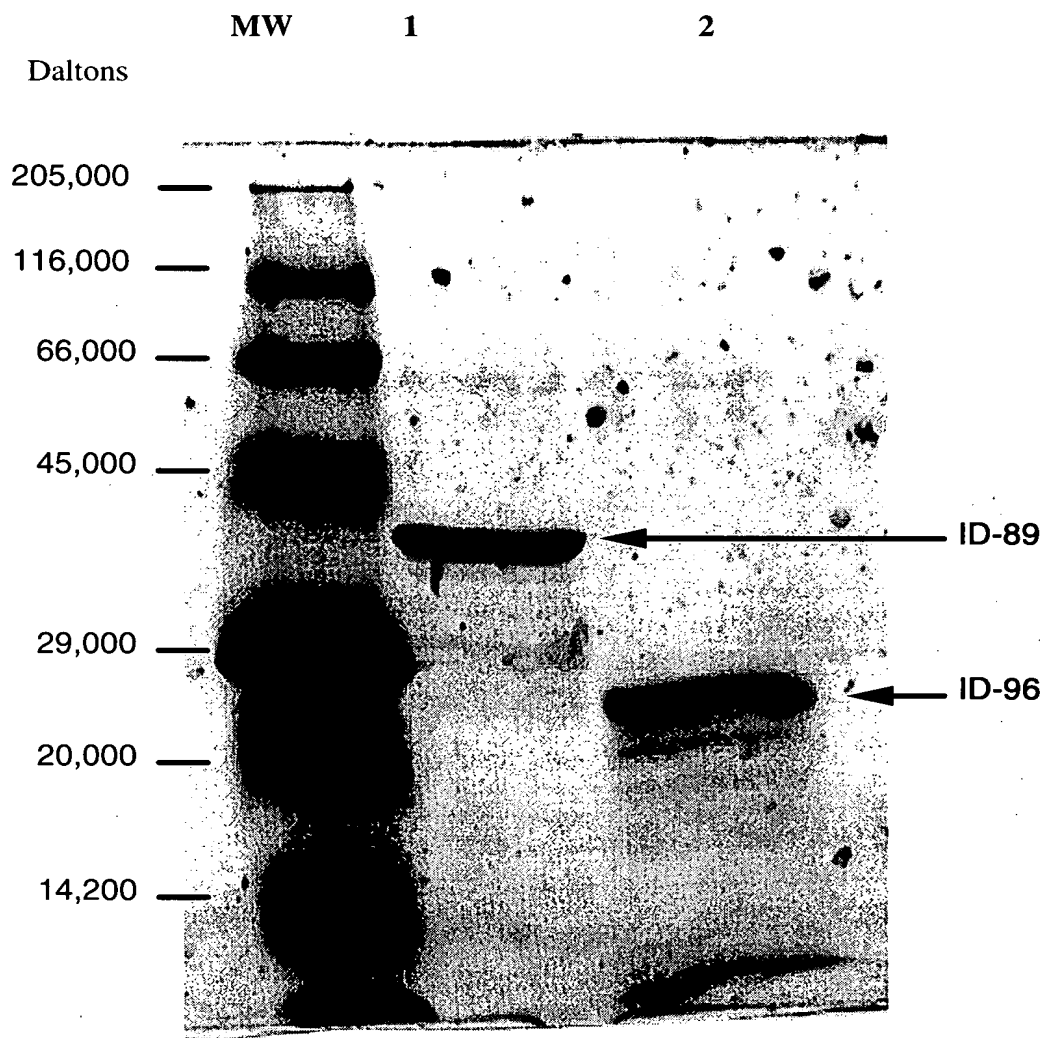


Figure 7

SDS-PAGE analysis of the purified ID-89 and ID-96 protein antigens

5



10

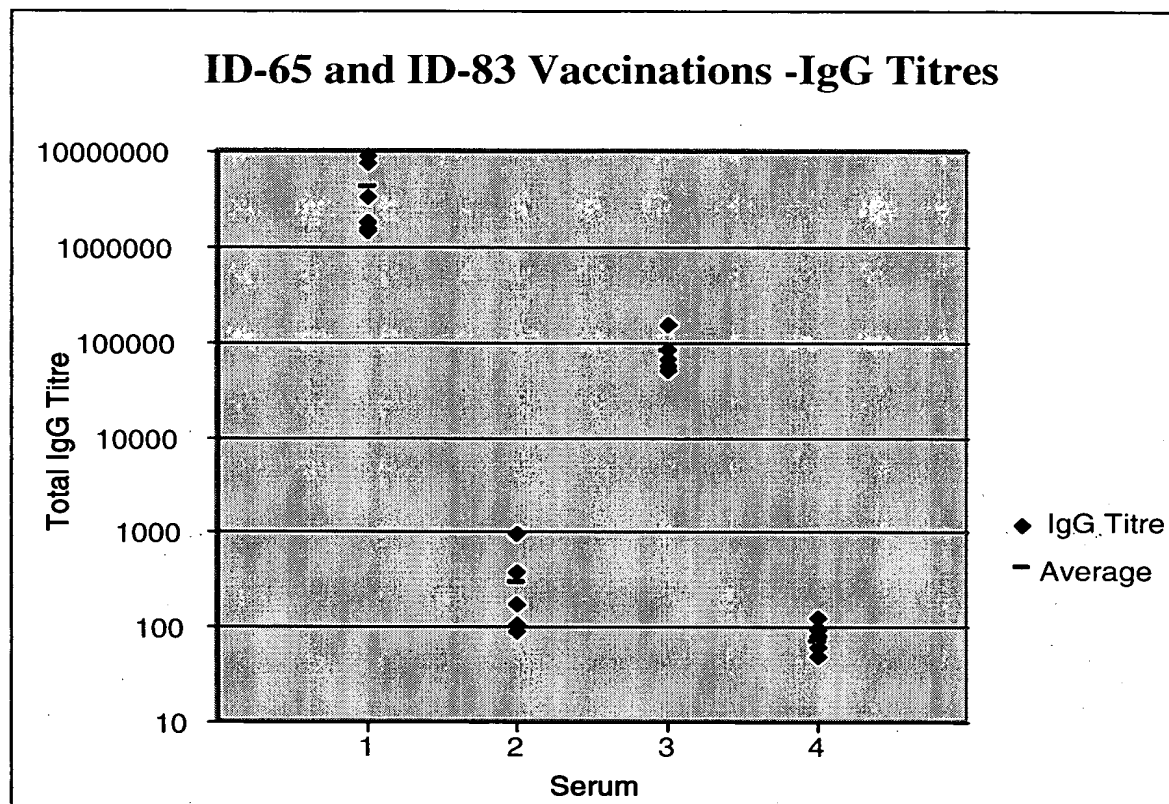




Figure 8

IgG Titres against the ID-65 and ID-83 Proteins

5



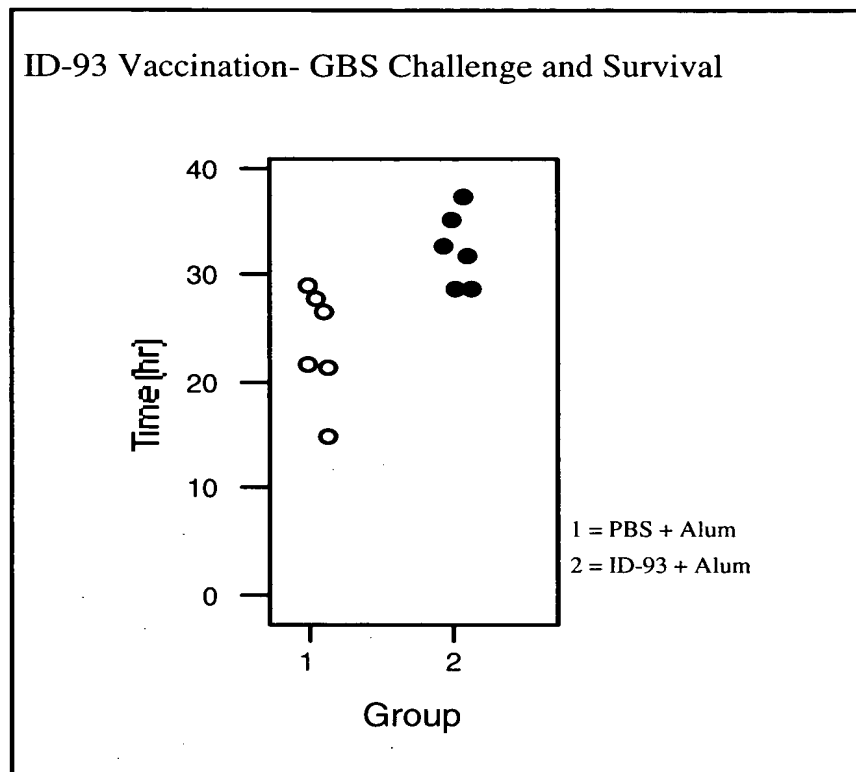
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15



Figure 9

Survival Data



5

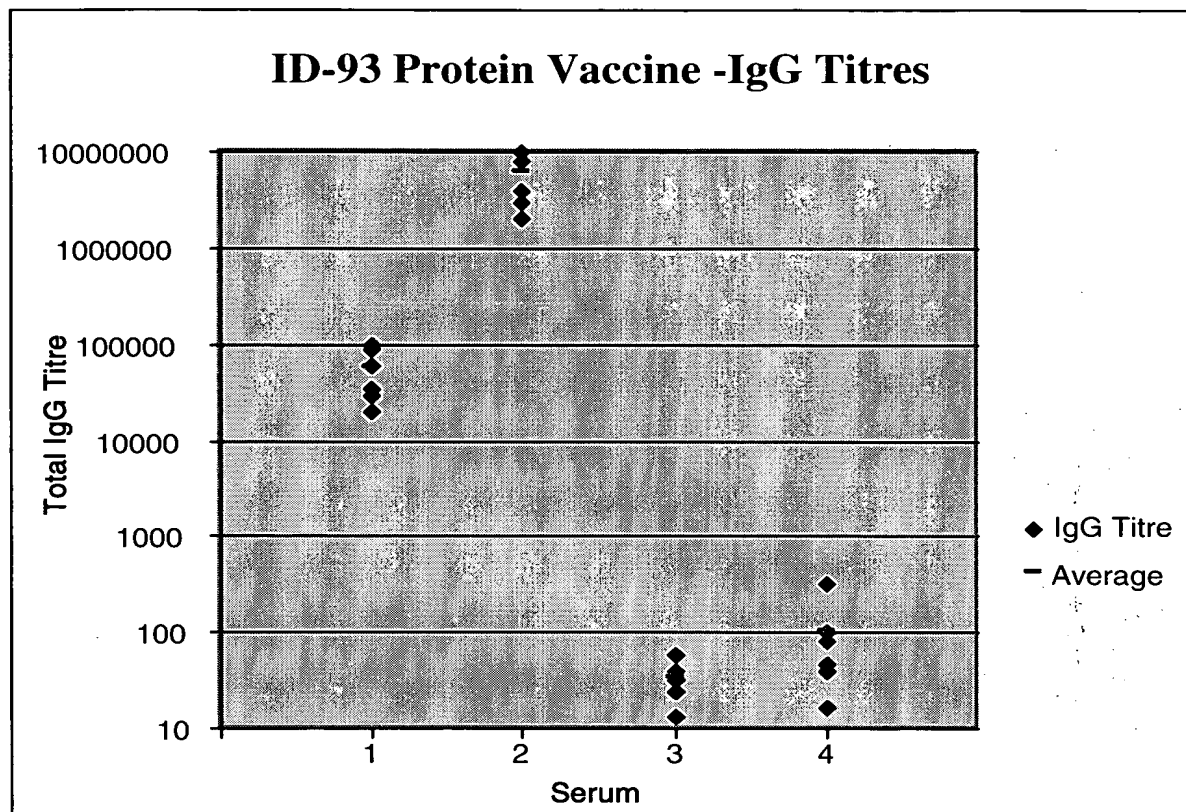
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Figure 10

IgG Titres against the ID-93 Protein

5





**Figure 13 Southern blot analysis – ID-65**

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

5

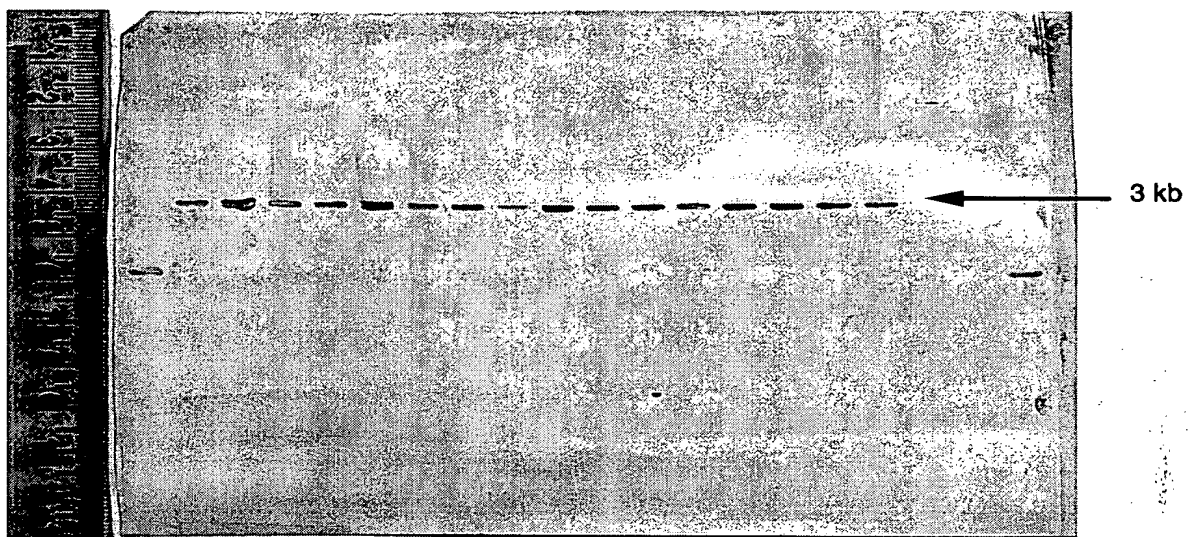




Figure 11

IgG Titres against the ID-89 and ID-96 Proteins

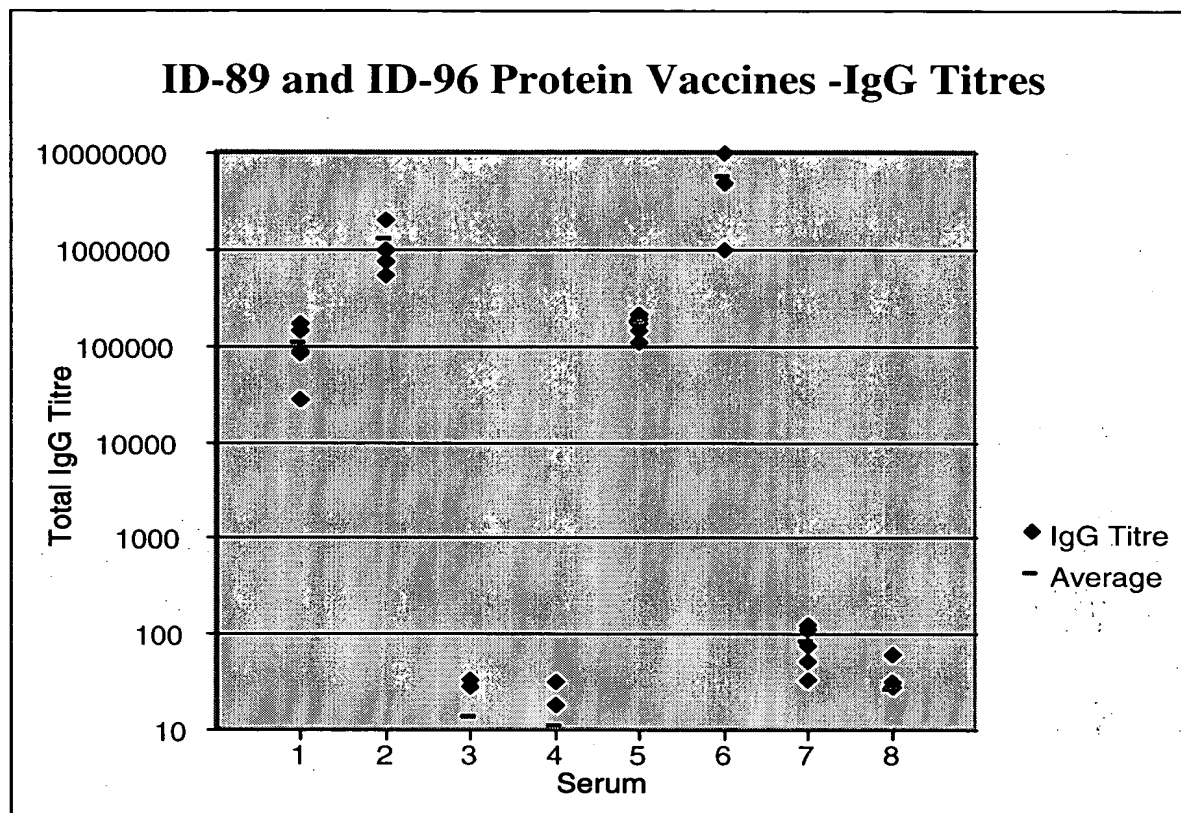
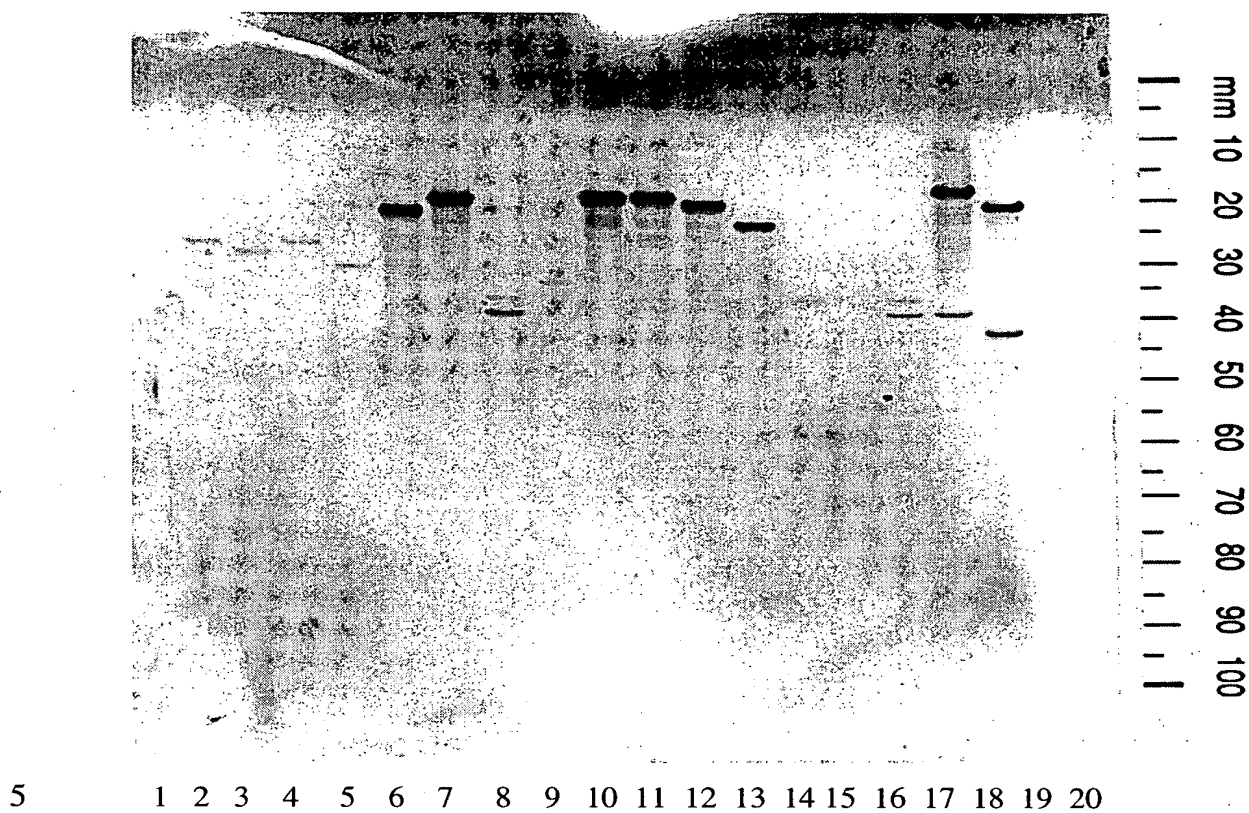




Figure 12

Southern blot analysis - *rib*



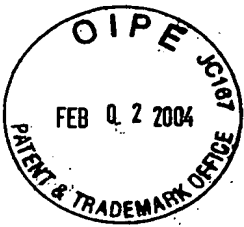
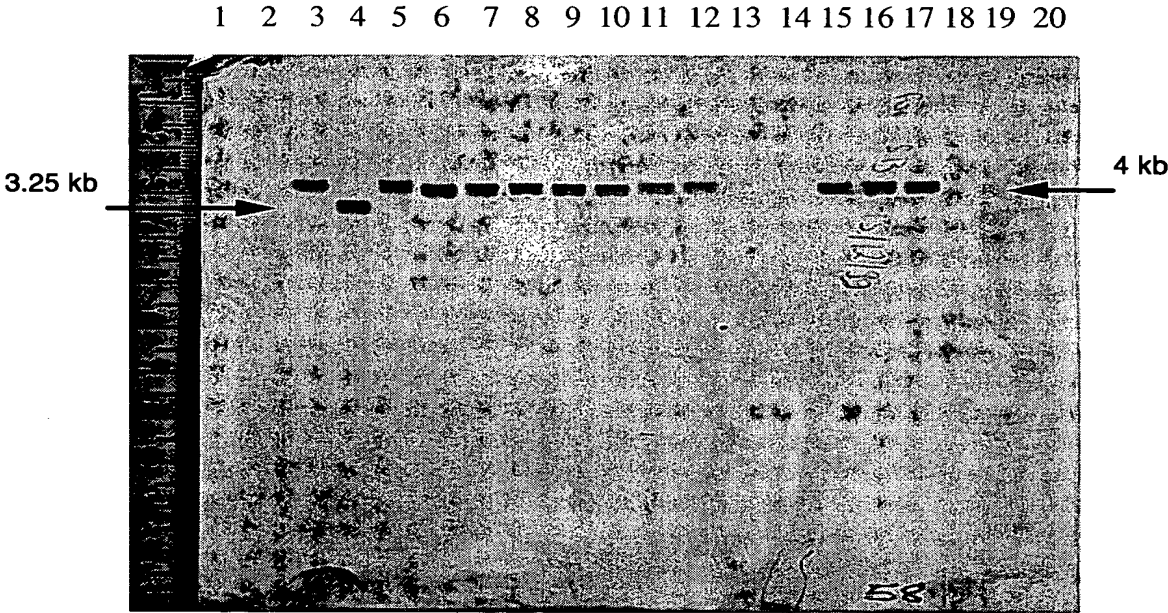


Figure 14

Southern blot analysis – ID-89

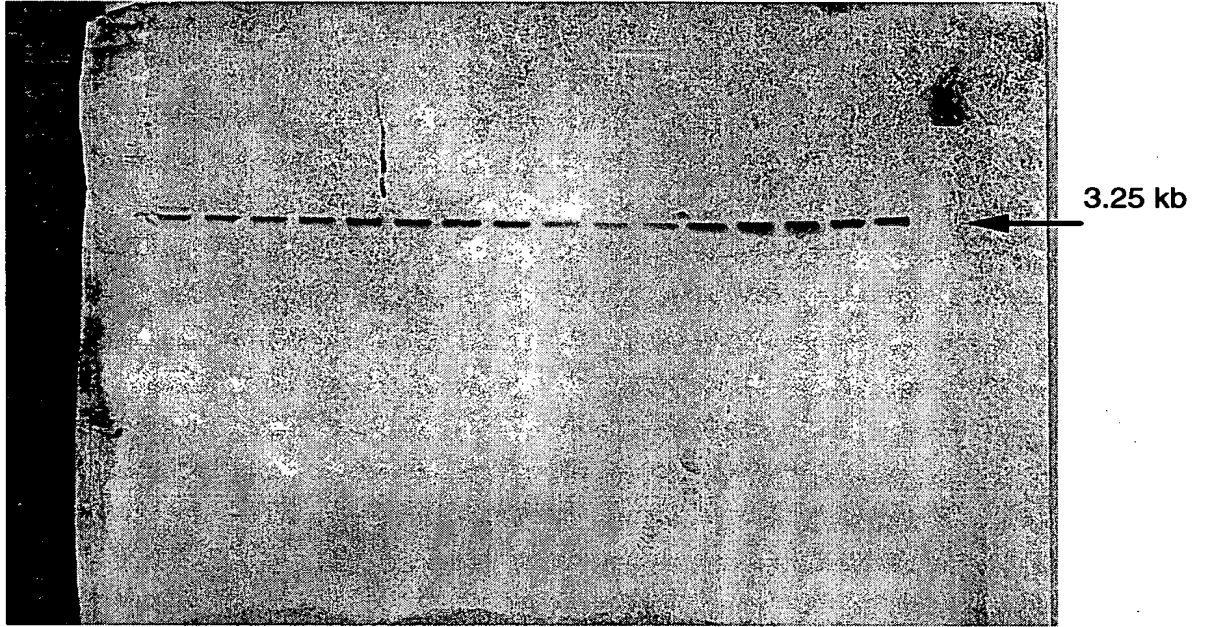




**Figure 15**

**Southern blot analysis – ID-93**

5                      1   2   3   4   5   6   7   8   9   10   11   12   13   14   15   16   17   18   19   20





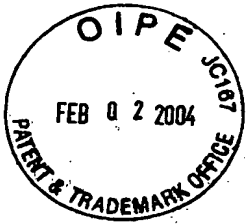


Figure 16 Southern blot analysis – ID-96

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

5

